

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:45:01 ; Search time 35 Seconds  
(without alignments)  
15.229 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 4  
Sequence: 1 KLVF 4

Scoring table: OLIGO  
Gapox 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

A\_Geneseq\_101002:\*  
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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	4	AAW45956	Beta-amyloid beta pepti
2	4	100.0	4	AAW79936	Anti-D peptide used
3	4	100.0	4	AAW82627	Anti-D peptide used
4	4	100.0	4	AAW82635	Anti-D peptide used
5	4	100.0	4	AAW84879	Anti-D peptide used
6	4	100.0	4	AAW84879	Anti-D peptide used
7	4	100.0	4	AAW96815	Anti-D peptide used
8	4	100.0	4	AAW96823	Anti-D peptide used
9	4	100.0	4	AAW11653	Anti-D peptide used
10	4	100.0	4	AAW11661	Anti-D peptide used

11	4	100.0	5	AAW87922	Test peptide used
12	4	100.0	5	AAW02313	Beta-amyloid modul
13	4	100.0	5	AAW45933	Partial sequence o
14	4	100.0	5	AAW45950	Amyloid beta pepti
15	4	100.0	5	AAW45966	Peptide derived fr
16	4	100.0	5	AAW29089	A-beta-binding pep
17	4	100.0	5	AAW89367	Beta-amyloid pepti
18	4	100.0	5	AAW79937	Beta-amyloid recog
19	4	100.0	5	AAW82629	All-D peptide used
20	4	100.0	5	AAW82637	All-D peptide used
21	4	100.0	5	AAW62803	Residues 16-20 of
22	4	100.0	5	AAW67279	Residues 16-20 of
23	4	100.0	5	AAW48481	Anti-fibrillogenic
24	4	100.0	5	AAW48489	Anti-fibrillogenic
25	4	100.0	5	AAW84001	Transglutaminase i
26	4	100.0	5	AAW96817	Amyloid targeting
27	4	100.0	5	AAW96825	Amyloid targeting
28	4	100.0	5	AAW11655	Peptide #8, used a
29	4	100.0	5	AAW11663	Peptide #16, used
30	4	100.0	5	AAW05158	Beta amyloid pepti
31	4	100.0	5	AAW05183	Beta amyloid pepti
32	4	100.0	6	AAW02331	Beta-amyloid modul
33	4	100.0	6	AAW02313	Beta-amyloid modul
34	4	100.0	6	AAW02314	Beta-amyloid modul
35	4	100.0	6	AAW45944	Amyloid beta pepti
36	4	100.0	6	AAW45945	Amyloid beta pepti
37	4	100.0	6	AAW29090	A-beta-binding pep
38	4	100.0	6	AAW29091	A-beta-binding pep
39	4	100.0	6	AAW29092	A-beta-binding pep
40	4	100.0	6	AAW89388	Beta-amyloid pepti
41	4	100.0	6	AAW89377	Beta-amyloid pepti
42	4	100.0	6	AAW89378	Beta-amyloid pepti
43	4	100.0	6	AAW82632	All-D peptide used
44	4	100.0	6	AAW82651	All-D peptide used
45	4	100.0	6	AAW82654	All-D peptide used
46	4	100.0	6	AAW82657	All-D peptide used
47	4	100.0	6	AAW82660	All-D peptide used
48	4	100.0	6	AAW82663	All-D peptide used
49	4	100.0	6	AAW84876	Anti-fibrillogenic
50	4	100.0	6	AAW84884	Anti-fibrillogenic
51	4	100.0	6	AAW84896	Anti-fibrillogenic
52	4	100.0	6	AAW83305	Amyloid-beta (Abet
53	4	100.0	6	AAW96820	Amyloid targeting
54	4	100.0	6	AAW11650	Peptide #3, used a
55	4	100.0	6	AAW11911	Peptide #24, used
56	4	100.0	6	AAW05156	Beta amyloid pepti
57	4	100.0	6	AAW05157	Beta amyloid pepti
58	4	100.0	6	AAW05157	Beta amyloid pepti
59	4	100.0	6	AAW05177	Beta amyloid pepti
60	4	100.0	6	AAW05189	Beta amyloid pepti
61	4	100.0	7	AAW45231	Beta amyloid prote
62	4	100.0	7	AAW87921	Test peptide used
63	4	100.0	7	AAW88300	Non-amyloid pepti
64	4	100.0	7	AAW02311	Beta-amyloid modul
65	4	100.0	7	AAW02312	Beta-amyloid modul
66	4	100.0	7	AAW45940	Amyloid beta pepti
67	4	100.0	7	AAW45941	Amyloid beta pepti
68	4	100.0	7	AAW89375	Beta-amyloid pepti
69	4	100.0	7	AAW89376	Beta-amyloid pepti
70	4	100.0	7	AAW82624	All-D peptide used
71	4	100.0	7	AAW82639	All-D peptide used
72	4	100.0	7	AAW82640	All-D peptide used
73	4	100.0	7	AAW67281	Residues 16-22 of
74	4	100.0	7	AAW48475	Anti-fibrillogenic
75	4	100.0	7	AAW48491	Anti-fibrillogenic
76	4	100.0	7	AAW48492	Anti-fibrillogenic
77	4	100.0	7	AAW96812	Amyloid targeting
78	4	100.0	7	AAW96827	Amyloid targeting
79	4	100.0	7	AAW96828	Amyloid targeting
80	4	100.0	7	AAW11649	Peptide #2, used a
81	4	100.0	7	AAW11655	Peptide #18, used
82	4	100.0	7	AAW11666	Peptide #19, used
83	4	100.0	7	AAW05154	Beta amyloid pepti

84	4	100.0	7	23	ABB05155	Beta amyloid pepti	157	4	100.0	22	15	AAR46967	J alpha sequence (
85	4	100.0	7	23	ABB04920	Human amyloid beta	158	4	100.0	23	17	AAR92446	lytic peptide used
86	4	100.0	8	16	AAR74104	P-selectin inhibit	159	4	100.0	23	17	AAR90003	Synthetic lytic pe
87	4	100.0	8	16	AAR74105	P-selectin inhibit	160	4	100.0	24	15	AAR52569	Alzheimer's diseas
88	4	100.0	8	16	AAR74099	P-selectin inhibit	161	4	100.0	25	22	ABB41687	Peptide #9193 enco
89	4	100.0	8	17	AAR02310	Beta-amyloid modul	162	4	100.0	25	22	AAM62560	Human brain expres
90	4	100.0	8	18	AAW45937	Amyloid beta pepti	163	4	100.0	25	22	AAM75371	Human bone marrow
91	4	100.0	8	18	AAW45938	Amyloid beta pepti	164	4	100.0	25	22	AAM35483	Peptide #9520 enco
92	4	100.0	8	18	AAW45967	Peptide derived fr	165	4	100.0	26	19	AAW56144	T cell receptor al
93	4	100.0	8	18	AAW32551	Amyloidogenic sequ	166	4	100.0	26	19	AAW47229	Beta-amyloid enco
94	4	100.0	8	20	AAW89374	Beta-amyloid pepti	167	4	100.0	26	20	AAW33408	Human amyloidogeni
95	4	100.0	8	22	AAE10663	Human amyloid prec	168	4	100.0	27	16	AAR80129	TCR CDR3 V-alpha r
96	4	100.0	8	23	AAE02615	Human amyloid prec	169	4	100.0	27	17	AAR92447	Lytic peptide used
97	4	100.0	8	23	ABB78624	Human alpha secret	170	4	100.0	27	17	AAR92448	Lytic peptide used
98	4	100.0	9	23	ABB05153	Beta amyloid pepti	171	4	100.0	27	17	AAR90004	Synthetic lytic pe
99	4	100.0	9	14	AAR45239	Mutant amyloid pre	172	4	100.0	27	17	AAR90005	Synthetic lytic pe
100	4	100.0	9	18	AAW45935	Amyloid beta pepti	173	4	100.0	27	20	AAW33409	Human amyloidogeni
101	4	100.0	9	18	AAW45936	Amyloid beta pepti	174	4	100.0	28	8	AAW70594	Sequence of Alzheimer
102	4	100.0	9	22	AAW48493	Antifibrillogenic	175	4	100.0	28	10	AAW90381	Synthetic A4 amylo
103	4	100.0	9	23	AAU11667	Peptide #20, used	176	4	100.0	28	15	AAR54702	Beta-amyloid fragm
104	4	100.0	9	23	ABB04913	Human amyloid beta	177	4	100.0	28	15	AAR60368	Beta-amyloid (1-28
105	4	100.0	10	18	AAW45934	Amyloid beta pepti	178	4	100.0	28	16	AAR64170	A4-O(1-28) a parti
106	4	100.0	10	21	AAW79938	Beta-amyloid recog	179	4	100.0	28	16	AAR64171	A4-P(1-28) a parti
107	4	100.0	10	22	AAW43319	Mycoplasma genital	180	4	100.0	28	16	AAR64172	A4-B(1-28) a parti
108	4	100.0	10	22	AAW82641	All-D peptide used	181	4	100.0	28	16	AAR64164	Generic beta amylo
109	4	100.0	10	22	AAW46222	Human APP derived	182	4	100.0	28	17	AAW01413	Beta/A4-amyloid pe
110	4	100.0	10	22	AAW46223	Human APP derived	183	4	100.0	28	17	AAW01414	Beta/A4-amyloid pe
111	4	100.0	10	22	AAW46224	Human APP derived	184	4	100.0	28	20	AAW39805	Beta-amyloid prote
112	4	100.0	10	22	AAW46225	Human APP derived	185	4	100.0	28	20	AAW81467	Synthetic amyloid
113	4	100.0	10	22	AAW46226	Human APP derived	186	4	100.0	28	22	AAW91783	Amyloid beta-prote
114	4	100.0	10	22	AAW46227	Human APP derived	187	4	100.0	28	22	AAW91789	Amyloid beta-prote
115	4	100.0	10	22	AAW46228	Human APP derived	188	4	100.0	28	22	AAW91800	Amyloid beta-prote
116	4	100.0	10	23	ABB84047	Transglutaminase i	189	4	100.0	28	22	AAW91816	Amyloid beta-prote
117	4	100.0	10	18	AAW96829	Amyloid targeting	190	4	100.0	28	22	AAW91827	Amyloid beta-prote
118	4	100.0	11	13	AAW32560	Anti-amyloid pepti	191	4	100.0	28	22	AAW49396	Human amyloid pept
119	4	100.0	11	21	AAW75943	Beta-amyloid hybri	192	4	100.0	28	22	AAW35590	Human clone B(1-28
120	4	100.0	11	22	AAW52586	Peptide #16 for il	193	4	100.0	28	22	AAW35591	Human clone DIN B(
121	4	100.0	11	22	AAW91781	Amyloid beta-prote	194	4	100.0	28	22	AAW35592	Human clone E3Q B(
122	4	100.0	11	22	AAW91787	Amyloid beta-prote	195	4	100.0	28	22	AAW35593	Human clone R5Q B(
123	4	100.0	11	22	AAW91814	Amyloid beta-prote	196	4	100.0	28	22	AAW35594	Human clone H6Q B(
124	4	100.0	11	23	AAW99431	Human amyloid beta	197	4	100.0	28	22	AAW35595	Human clone D7Q B(
125	4	100.0	12	21	AAW67849	Alpha-2 antiplasmi	198	4	100.0	28	22	AAW35596	Human clone E11Q B
126	4	100.0	14	21	AAW11773	Human oncoprotein	199	4	100.0	28	22	AAW35597	Human clone H13Q B
127	4	100.0	14	22	AAW96881	Human peptide #156	200	4	100.0	28	22	AAW35598	Human clone H14Q B
128	4	100.0	15	15	AAW49329	P. falcip. p190 po	201	4	100.0	28	22	AAW35600	Human clone E22Q B
129	4	100.0	15	17	AAW02334	Beta-amyloid pepti	202	4	100.0	28	22	AAW36201	Human clone D23Q B
130	4	100.0	15	17	AAW02333	Beta-amyloid pepti	203	4	100.0	28	22	AAW36202	Human clone X28Q B
131	4	100.0	15	19	AAW54717	Peptide from P.fal	204	4	100.0	28	23	AAW21439	Human beta-amyloid
132	4	100.0	15	20	AAW89353	Beta-amyloid pepti	205	4	100.0	28	23	AAW76030	Beta amyloid pepti
133	4	100.0	15	20	AAW89354	Beta-amyloid pepti	206	4	100.0	28	23	AAU76484	Amino acids 1-29 o
134	4	100.0	15	20	AAW89358	Beta-amyloid pepti	207	4	100.0	28	23	AAW50910	Beta amyloid prote
135	4	100.0	15	23	ABB05152	Beta amyloid pepti	208	4	100.0	28	23	ABB04910	Human amyloid beta
136	4	100.0	15	23	ABB05162	Beta amyloid pepti	209	4	100.0	30	20	AAW81468	Synthetic amyloid
137	4	100.0	16	10	AAW95052	Jx region encoded	210	4	100.0	30	22	ABB51151	Human secreted pro
138	4	100.0	16	10	AAW95054	Joining region enc	211	4	100.0	30	23	AAU11766	Human amyloid beta
139	4	100.0	17	13	AAR26959	Human T lymphocyte	212	4	100.0	32	22	AAW84430	Partial sequence o
140	4	100.0	17	15	AAR54703	Beta-amyloid fragm	213	4	100.0	33	20	AAW81469	Synthetic amyloid
141	4	100.0	17	18	AAW18880	Beta-amyloid pepti	214	4	100.0	33	21	AAW53620	Human colon cancer
142	4	100.0	17	22	AAW91774	Amyloid beta-prote	215	4	100.0	33	23	AAU93990	Human beta-amyloid
143	4	100.0	17	22	AAW91807	Amyloid beta-prote	216	4	100.0	34	22	ABB41895	Peptide #9401 enco
144	4	100.0	17	23	AAW48346	Beta-amyloid anti	217	4	100.0	34	22	AAM62773	Human brain expres
145	4	100.0	17	23	ABB04911	Human amyloid beta	218	4	100.0	34	22	AAW75589	Human bone marrow
146	4	100.0	18	21	AAW10963	Beta-amyloid precu	219	4	100.0	34	22	AAW87856	Human immune/haema
147	4	100.0	18	21	AAW10964	Beta-amyloid precu	220	4	100.0	34	22	AAW35696	Peptide #9733 enco
148	4	100.0	19	18	AAW18882	ADANS-beta-amyloi	221	4	100.0	35	17	AAW02335	Beta-amyloid pepti
149	4	100.0	19	18	AAW18881	Trp-Beta-amyloid p	222	4	100.0	35	17	AAW02336	Beta-amyloid pepti
150	4	100.0	19	19	AAW85066	Signal peptide for	223	4	100.0	35	19	AAW47228	Beta-amyloid pepti
151	4	100.0	19	21	AAW79935	Beta-amyloid inhib	224	4	100.0	35	20	AAW89355	Beta-amyloid pepti
152	4	100.0	19	22	AAW46201	Human APP A-beta 1	225	4	100.0	35	20	AAW89356	Beta-amyloid pepti
153	4	100.0	19	22	AAW49097	Human amyloid beta	226	4	100.0	35	20	AAW89357	Beta-amyloid pepti
154	4	100.0	20	21	AAW79934	Beta-amyloid inhib	227	4	100.0	35	20	AAW89359	Beta-amyloid pepti
155	4	100.0	20	23	ABB06431	Beta-secretase rel	228	4	100.0	35	20	AAW89361	Beta-amyloid pepti
156	4	100.0	21	20	AAW30941	Human secretase SE	229	4	100.0	35	22	AAW91803	Amyloid beta-prote

230	4	100.0	35	22	AAB91830	Amyloid beta-prote	303	4	100.0	42	19	AAW42989	Full length beta-a
231	4	100.0	35	23	ABE05163	Beta amyloid pepti	304	4	100.0	42	20	AAV49691	Human beta amyloid
232	4	100.0	35	23	ABE05164	EEVHHHQQ-Beta am	305	4	100.0	42	20	AAV33407	Human amyloidogeni
233	4	100.0	36	8	AAI70037	Secretory signal s	306	4	100.0	42	20	AAV25137	Human amyloid beta
234	4	100.0	36	20	AAW81471	Synthetic amyloid	307	4	100.0	42	20	AAV08607	Human beta-amyloid
235	4	100.0	36	23	AAU11771	Synthetic immunoge	308	4	100.0	42	20	AAW28093	A-beta-binding pep
236	4	100.0	36	23	AAU11776	Synthetic immunoge	309	4	100.0	42	20	AAW99585	Mutant aggregating
237	4	100.0	38	15	AAE60362	Beta-amyloid (1-38	310	4	100.0	42	20	AAW92726	Human tacyhkinin a
238	4	100.0	38	19	AAW74899	Human secreted pro	311	4	100.0	42	20	AAW81474	Human tacyhkinin a
239	4	100.0	38	20	AAW92722	Human tacyhkinin a	312	4	100.0	42	21	AAV96956	Synthetic amyloid
240	4	100.0	38	22	AAW91799	Amyloid beta-prote	313	4	100.0	42	22	AAW82622	Beta-amyloid 1-42
241	4	100.0	38	22	AAW91826	Amyloid beta-prote	314	4	100.0	42	22	AAE05484	Amyloid-beta pepti
242	4	100.0	39	15	AAE60363	Beta-amyloid (1-39	315	4	100.0	42	22	AAW84427	Human peptide anti
243	4	100.0	39	20	AAW25134	Human amyloid beta	316	4	100.0	42	22	AAE03425	Partial sequence o
244	4	100.0	39	20	AAW81472	Synthetic amyloid	317	4	100.0	42	22	AAW86134	Mouse amyloid prec
245	4	100.0	39	21	AAE69717	Beta-APP alpha-sec	318	4	100.0	42	22	AAW91779	Human Alzheimer-be
246	4	100.0	39	21	AAE69718	Beta-APP alpha-sec	319	4	100.0	42	22	AAW91785	Amyloid beta-prote
247	4	100.0	39	21	AAW52132	Human Receptor to	320	4	100.0	42	22	AAW91791	Amyloid beta-prote
248	4	100.0	40	14	AAW31391	Beta-amyloid pepti	321	4	100.0	42	22	AAW91812	Amyloid beta-prote
249	4	100.0	40	15	AAW60364	Beta-amyloid (1-40	322	4	100.0	42	22	AAW91818	Amyloid beta-prote
250	4	100.0	40	18	AAW37507	Amyloid beta prote	323	4	100.0	42	22	AAW48497	Human amyloid beta
251	4	100.0	40	18	AAW23335	Amyloid beta pepti	324	4	100.0	42	22	AAW48497	Human amyloid beta
252	4	100.0	40	19	AAW47232	Beta-amyloid pepti	325	4	100.0	42	22	AAW48830	Human amyloid beta
253	4	100.0	40	19	AAW47226	Beta-amyloid pepti	326	4	100.0	42	22	AAW49395	Human amyloid beta
254	4	100.0	40	20	AAW39339	Beta-amyloid pepti	327	4	100.0	42	22	AAW35589	Human amyloid pept
255	4	100.0	40	20	AAW39804	Beta-amyloid prote	328	4	100.0	42	22	AAU98727	Human amyloid beta
256	4	100.0	40	20	AAW25135	Human amyloid beta	329	4	100.0	42	23	AAW883306	Amyloid-beta (Abet
257	4	100.0	40	20	AAW14099	Human beta-amyloid	330	4	100.0	42	23	AAU96896	Human Amyloid beta
258	4	100.0	40	20	AAW9584	Wild type aggregat	331	4	100.0	42	23	AAW81321	Amyloid precursor
259	4	100.0	40	20	AAW92723	Human tacyhkinin a	332	4	100.0	42	23	AAE21438	Human beta-amyloid
260	4	100.0	40	20	AAW81473	Synthetic amyloid	333	4	100.0	42	23	AAW76029	Beta amyloid pepti
261	4	100.0	40	22	AAE05483	Human peptide anti	334	4	100.0	42	23	AAU93988	Human beta-amyloid
262	4	100.0	40	22	AAW84426	Partial sequence o	335	4	100.0	42	23	AAU75939	Humno acids 1-42 o
263	4	100.0	40	22	AAW84429	Amyloid beta-prote	336	4	100.0	42	23	AAU75939	Humno acids 1-42 o
264	4	100.0	40	22	AAW91780	Amyloid beta-prote	337	4	100.0	42	23	AAU80961	Human amyloid beta
265	4	100.0	40	22	AAW91786	Amyloid beta-prote	338	4	100.0	42	23	AAW68314	Human amyloid beta
266	4	100.0	40	22	AAW91792	Amyloid beta-prote	339	4	100.0	42	23	AAW51864	Human amyloid beta
267	4	100.0	40	22	AAW91802	Amyloid beta-prote	340	4	100.0	42	23	AAU75433	Neuronal death inh
268	4	100.0	40	22	AAW91813	Amyloid beta-prote	341	4	100.0	42	23	AAW96371	Amyloid peptide pr
269	4	100.0	40	22	AAW91819	Amyloid beta-prote	342	4	100.0	43	10	AAW96371	Region of pre-APC
270	4	100.0	40	22	AAW91829	Amyloid beta-prote	343	4	100.0	43	15	AAW54759	Beta amyloid pepti
271	4	100.0	40	23	AAU99425	Human amyloid beta	344	4	100.0	43	15	AAW60367	Beta-amyloid (1-43
272	4	100.0	40	23	AAE22990	Human amyloid-beta	345	4	100.0	43	15	AAW61328	Amyloid beta-prote
273	4	100.0	40	23	AAU96895	Human self-associa	346	4	100.0	43	16	AAW64165	Beta amyloid prote
274	4	100.0	40	23	AAW80186	Amyloid beta pepti	347	4	100.0	43	17	AAW95673	A-beta protein (43
275	4	100.0	40	23	AAW50909	Beta amyloid prote	348	4	100.0	43	18	AAW93371	Human beta-amyloid
276	4	100.0	40	23	AAU11772	Synthetic immunoge	349	4	100.0	43	19	AAW17758	Beta-amyloid pepti
277	4	100.0	40	23	AAU11773	Synthetic immunoge	350	4	100.0	43	19	AAW71378	Beta-amyloid pepti
278	4	100.0	40	23	AAW68313	Human beta amyloid	351	4	100.0	43	19	AAW51316	Natural beta-amylo
279	4	100.0	41	23	AAW51863	Human amyloid beta	352	4	100.0	43	19	AAW40129	Human amyloid-beta
280	4	100.0	41	13	AAW22306	Alzheimer's amyloi	353	4	100.0	43	20	AAW42955	Beta-amyloid-beta
281	4	100.0	41	15	AAW60365	Beta-amyloid (1-41	354	4	100.0	43	20	AAW92724	Human tacyhkinin a
282	4	100.0	41	16	AAW65283	Beta amyloid pepti	355	4	100.0	43	20	AAW89362	Beta-amyloid pepti
283	4	100.0	41	20	AAW25136	Human amyloid beta	356	4	100.0	43	21	AAW27020	Beta-amyloid pepti
284	4	100.0	41	20	AAW25136	Human amyloid beta	357	4	100.0	43	21	AAW21216	Human beta-amyloid
285	4	100.0	41	21	AAW81497	Lambda SMM9 beta-a	358	4	100.0	43	21	AAW88390	Beta-amyloid pepti
286	4	100.0	42	9	AAW83153	Beta-amyloid-relat	359	4	100.0	43	21	AAW56102	Beta-amyloid pepti
287	4	100.0	42	12	AAW10025	Sequence of A99 (b	360	4	100.0	43	21	AAW07901	Natural beta amylo
288	4	100.0	42	13	AAW33192	Beta-amyloid pepti	361	4	100.0	43	22	AAW07901	Beta-amyloid pepti
289	4	100.0	42	14	AAW33192	Beta-amyloid pepti	362	4	100.0	43	22	AAW07901	Human beta amyloid
290	4	100.0	42	14	AAW37867	Beta-amyloid prote	363	4	100.0	43	22	AAE12508	Beta-amyloid pepti
291	4	100.0	42	15	AAW60366	Beta-amyloid (1-42	364	4	100.0	43	22	AAU00291	Human steroid horm
292	4	100.0	42	16	AAW65284	Beta amyloid pepti	365	4	100.0	43	22	AAW84428	Human amyloid beta
293	4	100.0	42	16	AAW65285	Beta amyloid pepti	366	4	100.0	43	22	AAW89886	Beta-amyloid pepti
294	4	100.0	42	16	AAW65286	Beta amyloid pepti	367	4	100.0	43	22	AAW81193	Beta-amyloid pepti
295	4	100.0	42	16	AAW65287	Beta amyloid pepti	368	4	100.0	43	22	AAW91778	Beta-amyloid pepti
296	4	100.0	42	16	AAW65288	Beta amyloid pepti	369	4	100.0	43	22	AAW91811	Amyloid beta-prote
297	4	100.0	42	17	AAW95248	Beta/A4-amyloid pe	370	4	100.0	43	22	AAW47108	Biotinylated beta-
298	4	100.0	42	17	AAW9536	Murine beta amyloi	371	4	100.0	43	22	AAW48344	Beta-amyloid beta-
299	4	100.0	42	17	AAW88206	Rat A42 beta-amylo	372	4	100.0	43	23	AAU98701	Human amyloid beta
300	4	100.0	42	17	AAW94591	Alzheimer amyloid	373	4	100.0	43	23	AAW50862	Beta-amyloid pepti
301	4	100.0	42	18	AAW12828	Beta A4 peptide.	374	4	100.0	44	22	AAW05149	Beta amyloid pepti
302	4	100.0	42	19	AAW64507	Neurotoxic beta-am	375	4	100.0	44	22	AAW06420	Novel human diagno
	4	100.0	42	19	AAW47230	Beta-amyloid pepti				45	16	AAW64169	Variant beta amylo

376	4	100.0	45	22	AAW85918	Human immune/haema	449	4	100.0	70	22	AAE09374	Human APP695 Swedi
377	4	100.0	46	22	AAU20703	Human novel foetal	450	4	100.0	70	22	AAE09375	Human truncated AP
378	4	100.0	47	20	AAW81475	Synthetic amyloid	451	4	100.0	70	22	AAW79621	Human protein SEQ
379	4	100.0	48	21	AAAG1330	Arabidopsis thalia	452	4	100.0	70	22	AAU05015	Human amyloid prec
380	4	100.0	49	22	AAAB37523	Amyloid precursor	453	4	100.0	72	22	AAU17803	Novel human respir
381	4	100.0	48	21	AAAG1642	Arabidopsis thalia	454	4	100.0	73	21	AAAG22678	Zea mays protein f
382	4	100.0	50	20	AAAY2651	Brassica napus OSR	455	4	100.0	73	22	AAW24504	Clone CoSub-19 pre
383	4	100.0	50	22	AAAG65957	Human A4 amyloid p	456	4	100.0	73	22	AAAG99597	ERA binding domain
384	4	100.0	50	22	AAW83448	Human immune/haema	457	4	100.0	74	19	AAW61005	Streptococcus pneu
385	4	100.0	50	22	AAAB64819	Human secreted pro	458	4	100.0	75	21	AAAY55674	H. pylori ycfB pep
386	4	100.0	51	22	AAU43846	Propionibacterium	459	4	100.0	75	22	AAW90691	Human immune/haema
387	4	100.0	52	16	AAAG4166	Variant beta amylo	460	4	100.0	78	22	AAU14619	Novel bone marrow
388	4	100.0	52	20	AAW81476	Synthetic amyloid	461	4	100.0	78	22	AAW74136	Human colon cancer
389	4	100.0	52	23	ABP06943	Human ORFX protein	462	4	100.0	79	19	AAW53981	Human ALZASP. Hom
390	4	100.0	53	15	AAAS5695	Sequence of uniden	463	4	100.0	81	21	AAAB18232	Plasmodium falcipa
391	4	100.0	53	15	AAAS5696	Sequence of uniden	464	4	100.0	81	22	AAW96325	Human reproductive
392	4	100.0	53	16	AAAS5697	Sequence of uniden	465	4	100.0	82	22	AAO11351	Human polypeptide
393	4	100.0	53	15	AAAG4168	Variant beta amylo	466	4	100.0	82	22	AAW25544	Human protein sequ
394	4	100.0	53	21	AAAY87944	Mammalian amyloid	467	4	100.0	82	23	ABP00713	Human ORFX protein
395	4	100.0	53	22	AAW83959	Human immune/haema	468	4	100.0	82	23	AAU80960	Human amyloid beta
396	4	100.0	54	21	AAAB32126	Amyloid-beta precu	469	4	100.0	83	22	AAU55144	Propionibacterium
397	4	100.0	54	22	AAAB44245	Peptide #11751 enc	470	4	100.0	83	22	ABB10139	Human cDNA SEQ ID
398	4	100.0	54	22	ABW27119	Protein #9118 enco	471	4	100.0	83	22	AAO10377	Human polypeptide
399	4	100.0	54	22	AAW65283	Human brain expres	472	4	100.0	84	20	AAW89863	Human polypeptide
400	4	100.0	54	22	AAW77982	Human bone marrow	473	4	100.0	86	21	AAAG33173	Antigen 2 from cl
401	4	100.0	54	22	AAW21876	Peptide #8310 enco	474	4	100.0	87	21	AAAG26006	Zea mays protein f
402	4	100.0	54	22	AAW38202	Peptide #12239 enc	475	4	100.0	87	23	ABP03364	Zea mays protein f
403	4	100.0	54	23	ABG46998	Human peptide enco	476	4	100.0	88	21	AAAG14951	Human ORFX protein
404	4	100.0	55	22	ABW28623	Peptide #1274 enco	477	4	100.0	89	20	AAV12437	Arabidopsis thalia
405	4	100.0	55	22	ABW33806	Peptide #1312 enco	478	4	100.0	89	22	AAW91320	Human 5' EST secre
406	4	100.0	55	22	ABW19249	Protein #1248 enco	479	4	100.0	90	20	AAV12332	Human immune/haema
407	4	100.0	55	22	AAE12903	Human beta-amyloid	480	4	100.0	90	21	AAAG51282	Amino acid sequenc
408	4	100.0	55	22	AAW54572	Human brain expres	481	4	100.0	90	23	AAO21303	Arabidopsis thalia
409	4	100.0	55	22	AAW66979	Human bone marrow	482	4	100.0	90	23	AAO21304	Soybean KCP-like p
410	4	100.0	55	22	AAW14839	Peptide #1273 enco	483	4	100.0	91	20	AAV20121	Soybean KCP-like p
411	4	100.0	55	22	AAW27266	Peptide #1303 enco	484	4	100.0	91	22	ABG10961	B. burgdorferi ant
412	4	100.0	55	22	AAW25584	Peptide #1246 enco	485	4	100.0	91	22	AAO04130	Novel human diagn
413	4	100.0	55	22	AAAB11482	Human APP peptide	486	4	100.0	91	23	AAW49120	Human polypeptide
414	4	100.0	55	23	ABG36636	Human peptide enco	487	4	100.0	92	22	AAU17343	Human L-3-phosphos
415	4	100.0	56	19	AAW59651	Amino acid sequenc	488	4	100.0	92	22	ABG19083	Novel signal trans
416	4	100.0	56	22	AAW90698	Human BV123 16 pr	489	4	100.0	93	22	ABP07933	Novel human diagn
417	4	100.0	57	21	AAAB10910	Human amyloid prec	490	4	100.0	94	23	ABP07933	Human ORFX protein
418	4	100.0	58	20	AAW98001	Swedish-FAD APF714	491	4	100.0	95	20	AAV60235	Human endometrium
419	4	100.0	59	17	AAW05375	Amyloid precursor	492	4	100.0	96	18	AAV11318	S. pneumoniae poss
420	4	100.0	59	19	AAW70863	Beta-amyloid precu	493	4	100.0	96	20	AAV07859	Human secreted pro
421	4	100.0	59	22	AAW84425	Partial sequence o	494	4	100.0	96	21	AAAG33172	Zea mays protein f
422	4	100.0	60	19	AAW49007	Homo sapiens beta-	495	4	100.0	97	9	AAW81517	Deduced sequence o
423	4	100.0	60	21	AAV69701	Beta-amyloid precu	496	4	100.0	97	9	AAW83152	Lambda SM2W3 encod
424	4	100.0	60	22	AAU47183	Propionibacterium	497	4	100.0	97	14	AAW37865	Beta-amyloid prote
425	4	100.0	60	23	AAE21035	Gerbera sp. dihydr	498	4	100.0	97	19	AAW98414	H. pylori GHPO 96
426	4	100.0	61	21	AAAG00831	Human secreted pro	499	4	100.0	97	21	AAAG41574	H. pylori GHPO 284
427	4	100.0	61	22	AAU65140	Propionibacterium	500	4	100.0	97	21	AAAG49779	Arabidopsis thalia
428	4	100.0	62	21	AAW55001	Arabidopsis thalia	501	4	100.0	98	22	AAO01696	Arabidopsis thalia
429	4	100.0	62	23	ABP26179	Streptococcus poly	502	4	100.0	98	13	AAW20329	Human polypeptide
430	4	100.0	63	18	AAW26511	Amyloid precursor	503	4	100.0	99	16	AAW64167	Sequence of A99 (b
431	4	100.0	63	18	AAW26391	Amyloid precursor	504	4	100.0	99	16	AAW74694	Variant beta amylo
432	4	100.0	63	19	AAW44747	APP-REP 751 BAP pe	505	4	100.0	99	16	AAW74695	Beta-amyloid precu
433	4	100.0	63	19	AAW44746	APP-REP 751 (BAP E	506	4	100.0	99	16	AAW74696	Beta-amyloid precu
434	4	100.0	63	19	AAW42975	Beta-amyloid pepti	507	4	100.0	99	20	AAW08606	Human beta-amyloid
435	4	100.0	63	19	AAW42976	Beta-amyloid pepti	508	4	100.0	99	21	AAW34364	Human beta-amyloid
436	4	100.0	63	22	AAW94687	Human reproductive	509	4	100.0	99	21	AAW59822	Arabidopsis thalia
437	4	100.0	64	20	AAV27604	Human secreted pro	510	4	100.0	99	22	AAW88915	Arabidopsis thalia
438	4	100.0	64	23	ABW84366	Human immune/haema	511	4	100.0	99	22	AAO05699	Human immune/haema
439	4	100.0	64	23	ABW81320	Amyloid precursor	512	4	100.0	99	22	AAAB11483	Human APP peptide
440	4	100.0	65	22	AAU20974	Human novel foetal	513	4	100.0	99	23	ABW76945	Human polypeptide
441	4	100.0	65	22	AAU22225	Human cardiovascular	514	4	100.0	100	12	AAE10024	Amyloid Precursor
442	4	100.0	66	22	AAO02311	Human polypeptide	515	4	100.0	100	14	AAE10024	Beta-amyloid-relat
443	4	100.0	66	23	ABP00818	Human ORFX protein	516	4	100.0	100	21	AAE13015	Full-length beta-a
444	4	100.0	67	19	AAW71377	Peptide derived fr	517	4	100.0	100	21	AAE13015	Human amyloid prec
445	4	100.0	68	22	ABW16899	Human nervous syst	518	4	100.0	100	23	AAE14371	Transgenic APP pro
446	4	100.0	69	21	AAAG10885	Arabidopsis thalia	519	4	100.0	100	23	AAE14372	Amyloid precursor
447	4	100.0	69	23	ABP06650	Human ORFX protein	520	4	100.0	100	23	AAE14373	Amyloid precursor
448	4	100.0	70	22	AAE09373	Human wild-type AP	521	4	100.0	100	23	AAE14374	Amyloid precursor



522	4	100.0	100	23	AAE14375	Amyloid precursor	595	4	100.0	126	22	AAO10062	Human polypeptide
523	4	100.0	100	23	AAE14376	Amyloid precursor	596	4	100.0	127	16	AAE14376	Vipera palestinae
524	4	100.0	100	23	AAE14377	Amyloid precursor	597	4	100.0	127	21	AAE14377	Arbidopsis thalia
525	4	100.0	101	20	AAE14378	Protein involved i	598	4	100.0	127	21	AAE14378	Arbidopsis thalia
526	4	100.0	101	22	AAE14379	Human polypeptide	599	4	100.0	127	22	AAE14379	Human G protein-co
527	4	100.0	101	22	AAE14380	Human polypeptide	600	4	100.0	127	22	AAE14380	Human polypeptide
528	4	100.0	102	22	AAE14381	Physcomitrella pat	601	4	100.0	127	23	AAE14381	Novel G protein co
529	4	100.0	102	23	AAE14382	Human ORFX protein	602	4	100.0	127	23	AAE14382	Novel human chemok
530	4	100.0	103	16	AAE14383	Beta-amyloid precu	603	4	100.0	128	22	AAE14383	Human T2R35 amino
531	4	100.0	103	16	AAE14384	Beta-amyloid precu	604	4	100.0	128	23	AAE14384	Lactococcus lactis
532	4	100.0	103	19	AAE14385	Natural beta-amylo	605	4	100.0	130	18	AAE14385	H. pylori secreted
533	4	100.0	103	20	AAE14386	Beta-amyloid pepit	606	4	100.0	131	21	AAE14386	Arbidopsis thalia
534	4	100.0	103	21	AAE14387	Beta amyloid precu	607	4	100.0	131	22	AAE14387	Novel human diagno
535	4	100.0	103	22	AAE14388	Beta-amyloid precu	608	4	100.0	132	16	AAE14388	Rat beta amyloid f
536	4	100.0	103	23	AAE14389	Beta amyloid precu	609	4	100.0	132	16	AAE14389	Human beta amyloid
537	4	100.0	104	19	AAE14390	Amino acid sequenc	610	4	100.0	132	21	AAE14390	Arbidopsis thalia
538	4	100.0	105	22	AAE14391	Propionibacterium	611	4	100.0	132	21	AAE14391	Arbidopsis thalia
539	4	100.0	106	22	AAE14392	Novel human diagno	612	4	100.0	132	22	AAE14392	Drosophila melanog
540	4	100.0	106	22	AAE14393	Novel human diagno	613	4	100.0	132	23	AAE14393	Human ORFX protein
541	4	100.0	106	22	AAE14394	Human colon cancer	614	4	100.0	133	21	AAE14394	S. zoocapdemicus g
542	4	100.0	107	22	AAE14395	Lactococcus lactis	615	4	100.0	133	21	AAE14395	Arbidopsis thalia
543	4	100.0	108	9	AAE14396	Plasmid pARCP118-3	616	4	100.0	134	22	AAE14396	Drosophila melanog
544	4	100.0	108	14	AAE14397	Beta-amyloid-relat	617	4	100.0	135	21	AAE14397	Human ORFX ORF292
545	4	100.0	108	21	AAE14398	Zea mays protein f	618	4	100.0	135	21	AAE14398	Arbidopsis thalia
546	4	100.0	108	21	AAE14399	Human transmembran	619	4	100.0	135	22	AAE14399	Human polypeptide
547	4	100.0	108	23	AAE14400	Gamma-secretase su	620	4	100.0	135	23	AAE14400	Human ORFX protein
548	4	100.0	108	23	AAE14401	Gamma-secretase su	621	4	100.0	136	19	AAE14401	S. pneumoniae deri
549	4	100.0	108	23	AAE14402	Gamma-secretase su	622	4	100.0	140	21	AAE14402	Fatty acid biosynt
550	4	100.0	108	23	AAE14403	Gamma-secretase su	623	4	100.0	140	21	AAE14403	Arbidopsis thalia
551	4	100.0	108	23	AAE14404	Gamma-secretase su	624	4	100.0	140	22	AAE14404	Streptococcus thali
552	4	100.0	108	23	AAE14405	Gamma-secretase su	625	4	100.0	140	22	AAE14405	CER 10 protein seq
553	4	100.0	108	23	AAE14406	Gamma-secretase su	626	4	100.0	140	23	AAE14406	Streptococcus poly
554	4	100.0	109	23	AAE14407	Staphylococcus epi	627	4	100.0	140	23	AAE14407	Streptococcus poly
555	4	100.0	110	21	AAE14408	Arbidopsis thalia	628	4	100.0	142	21	AAE14408	Arbidopsis thalia
556	4	100.0	110	22	AAE14409	Human polypeptide	629	4	100.0	142	22	AAE14409	Human SLIT-2 homol
557	4	100.0	111	22	AAE14410	Human gastric canc	630	4	100.0	144	19	AAE14410	Pyroline-5-carbox
558	4	100.0	111	23	AAE14411	Human replicatio	631	4	100.0	144	23	AAE14411	Lactococcus lactis
559	4	100.0	112	17	AAE14412	Familial Alzheimer	632	4	100.0	145	22	AAE14412	Novel human neopl
560	4	100.0	112	20	AAE14413	PHIV-CAT chemokine	633	4	100.0	148	22	AAE14413	Human PRO polypept
561	4	100.0	113	22	AAE14414	Propionibacterium	634	4	100.0	148	23	AAE14414	Human polypeptide
562	4	100.0	115	20	AAE14415	Swedish-FAD APP po	635	4	100.0	149	21	AAE14415	Human ORFX ORF160
563	4	100.0	115	20	AAE14416	London-FAD APP po	636	4	100.0	149	21	AAE14416	Human cancer assoc
564	4	100.0	115	20	AAE14417	SwedishLondon-FAD	637	4	100.0	149	21	AAE14417	Arbidopsis thalia
565	4	100.0	115	21	AAE14418	Arbidopsis thalia	638	4	100.0	149	21	AAE14418	Arbidopsis thalia
566	4	100.0	116	21	AAE14419	Arbidopsis thalia	639	4	100.0	149	21	AAE14419	Arbidopsis thalia
567	4	100.0	116	21	AAE14420	Arbidopsis thalia	640	4	100.0	151	22	AAE14420	Novel human diagno
568	4	100.0	116	21	AAE14421	Arbidopsis thalia	641	4	100.0	151	23	AAE14421	Streptococcus poly
569	4	100.0	116	21	AAE14422	Arbidopsis thalia	642	4	100.0	151	23	AAE14422	Streptococcus thali
570	4	100.0	116	21	AAE14423	Human APP signal p	643	4	100.0	152	21	AAE14423	Arbidopsis thalia
571	4	100.0	117	19	AAE14424	Flag-amyloid prote	644	4	100.0	153	21	AAE14424	Arbidopsis thalia
572	4	100.0	117	21	AAE14425	Arbidopsis thalia	645	4	100.0	153	21	AAE14425	Arbidopsis thalia
573	4	100.0	117	21	AAE14426	Transgenic APP pro	646	4	100.0	153	21	AAE14426	Arbidopsis thalia
574	4	100.0	117	22	AAE14427	Human recombinant	647	4	100.0	154	21	AAE14427	Arbidopsis thalia
575	4	100.0	117	23	AAE14428	Human polypeptide	648	4	100.0	154	21	AAE14428	Arbidopsis thalia
576	4	100.0	118	19	AAE14429	APP C-terminal fra	649	4	100.0	155	21	AAE14429	Arbidopsis thalia
577	4	100.0	118	19	AAE14430	APP C-terminal fra	650	4	100.0	155	21	AAE14430	Arbidopsis thalia
578	4	100.0	118	19	AAE14431	APP C-terminal fra	651	4	100.0	155	22	AAE14431	Novel human enzyme
579	4	100.0	118	19	AAE14432	APP C-terminal fra	652	4	100.0	157	21	AAE14432	Arbidopsis thalia
580	4	100.0	118	19	AAE14433	APP C-terminal fra	653	4	100.0	157	22	AAE14433	Drosophila melanog
581	4	100.0	118	20	AAE14434	Amyloid precursor	654	4	100.0	158	21	AAE14434	Eucalyptus grandis
582	4	100.0	118	22	AAE14435	Human immune/haema	655	4	100.0	158	21	AAE14435	Arbidopsis thalia
583	4	100.0	120	19	AAE14436	S. pneumoniae poss	656	4	100.0	158	21	AAE14436	Arbidopsis thalia
584	4	100.0	120	19	AAE14437	APP C-terminal fra	657	4	100.0	159	19	AAE14437	H. pylori ORF hp4e
585	4	100.0	120	22	AAE14438	Human contig polyp	658	4	100.0	159	19	AAE14438	H. pylori GHP 762
586	4	100.0	121	23	AAE14439	Human ribosomal pr	659	4	100.0	159	21	AAE14439	Arbidopsis thalia
587	4	100.0	122	21	AAE14440	Beta-amyloid rubre	660	4	100.0	159	22	AAE14440	Human colon cancer
588	4	100.0	123	17	AAE14441	T-cell specific pe	661	4	100.0	159	22	AAE14441	H. pylori HPS083 p
589	4	100.0	123	21	AAE14442	Arbidopsis thalia	662	4	100.0	159	22	AAE14442	H. pylori HPC083 p
590	4	100.0	124	21	AAE14443	Beta-amyloid rubre	663	4	100.0	159	23	AAE14443	Listeria monocyoc
591	4	100.0	124	21	AAE14444	Arbidopsis thalia	664	4	100.0	160	22	AAE14444	Streptococcus pneu
592	4	100.0	125	20	AAE14445	B. burgdorferi ant	665	4	100.0	162	21	AAE14445	Amino acid sequenc
593	4	100.0	126	21	AAE14446	Arbidopsis thalia	666	4	100.0	162	21	AAE14446	Arbidopsis thalia
594	4	100.0	126	21	AAE14447	Arbidopsis thalia	667	4	100.0	163	18	AAE14447	Human colon specif

668	4	100.0	163	19	AAW46880	Protein sequence e	741	4	100.0	208	21	AAW83398	WTH3 C-terminal fr
669	4	100.0	163	20	AAU34758	Chlamydia pneumoniae	742	4	100.0	208	21	AAW83399	RAB6 polypeptide.
670	4	100.0	163	23	AAU76209	Human colon specif	743	4	100.0	208	21	AAW83400	RAB6C polypeptide.
671	4	100.0	164	21	AAW43336	Human ORFX ORF3100	744	4	100.0	208	21	AAW83403	RAB6C polypeptide.
672	4	100.0	164	22	AAU35818	Helicobacter pylori	745	4	100.0	208	22	ABW62513	Drosophila melanog
673	4	100.0	164	22	AAU35980	Helicobacter pylori	746	4	100.0	208	22	AAW78594	Human protein SEQ
674	4	100.0	166	22	AAU09762	Human polypeptide	747	4	100.0	208	22	AAU19215	Human G protein-co
675	4	100.0	167	19	AAW80477	Protein encoded by	748	4	100.0	209	21	AAW29317	Arabidopsis thalia
676	4	100.0	167	20	AAU03234	Clone HP01738 of a	749	4	100.0	209	23	AAW29476	Human G protein-co
677	4	100.0	167	20	AAU03235	Clone HP01738 of a	750	4	100.0	209	23	ABW60764	Novel G protein co
678	4	100.0	167	22	AAE12415	Albumin fusion pro	751	4	100.0	210	21	AAW05411	Arabidopsis thalia
679	4	100.0	168	22	ABG23504	Novel human diagno	752	4	100.0	210	21	AAW42942	Arabidopsis thalia
680	4	100.0	169	10	AAW95102	Joining and consta	753	4	100.0	210	22	AAU30856	Novel human secret
681	4	100.0	169	21	AAW07813	Amino acid sequenc	754	4	100.0	212	22	AAU31037	Novel human secret
682	4	100.0	169	22	AAU30339	Novel human secret	755	4	100.0	212	22	AAW11478	Arabidopsis thalia
683	4	100.0	169	22	AAW02522	Human digestive sy	756	4	100.0	213	22	AAW62541	B. melitensis viru
684	4	100.0	170	20	AAU35729	Amino acid sequenc	757	4	100.0	214	21	AAW23164	Arabidopsis thalia
685	4	100.0	170	23	ABW33546	Herbicidally activ	758	4	100.0	214	21	AAW31419	Arabidopsis thalia
686	4	100.0	172	22	AAU91367	Human G protein-co	759	4	100.0	214	22	AAW13786	Human polypeptide
687	4	100.0	172	23	ABW30437	Streptococcus poly	760	4	100.0	214	23	ABW26509	Streptococcus poly
688	4	100.0	172	23	ABW89556	Human polypeptide	761	4	100.0	215	21	AAW15861	Arabidopsis thalia
689	4	100.0	173	23	AAU56211	Propionibacterium	762	4	100.0	215	21	AAW21896	Arabidopsis thalia
690	4	100.0	173	23	ABW60933	Novel floral meris	763	4	100.0	215	21	AAW52998	Arabidopsis thalia
691	4	100.0	173	23	ABW60940	Novel floral meris	764	4	100.0	216	22	AAU48197	Propionibacterium
692	4	100.0	175	21	AAW83402	WTH3 fragment. HO	765	4	100.0	217	22	AAW56786	Human prostate can
693	4	100.0	176	21	AAW08453	Arabidopsis thalia	766	4	100.0	217	22	ABW60863	Drosophila melanog
694	4	100.0	176	22	AAW94210	Human protein sequ	767	4	100.0	219	22	AAU15993	Polypeptide p190-1
695	4	100.0	178	21	AAW32086	Arabidopsis thalia	768	4	100.0	219	22	AAW88498	Human novel secret
696	4	100.0	181	10	AAW91163	Kunitz-type trypsi	769	4	100.0	219	22	AAW51429	Haemophilus influe
697	4	100.0	182	21	AAW41596	Human ORFX ORF1360	770	4	100.0	219	23	AAW91429	Haemophilus influe
698	4	100.0	182	22	AAU87195	Novel central nerv	771	4	100.0	220	23	ABW28263	Streptococcus poly
699	4	100.0	183	22	AAW70764	A. gossypii isocit	772	4	100.0	220	23	ABW28264	Streptococcus poly
700	4	100.0	185	20	AAW35491	Chlamydia pneumoniae	773	4	100.0	221	21	AAW11081	Arabidopsis thalia
701	4	100.0	186	21	AAW11892	Arabidopsis thalia	774	4	100.0	221	21	AAW39743	Arabidopsis thalia
702	4	100.0	187	23	ABW30454	Streptococcus poly	775	4	100.0	221	22	AAU31856	Novel human secret
703	4	100.0	190	21	AAW16435	Arabidopsis thalia	776	4	100.0	224	18	AAW20154	H. pylori transpor
704	4	100.0	190	21	AAW32085	Arabidopsis thalia	777	4	100.0	224	18	AAW09640	Murine cytokine, S
705	4	100.0	191	12	AAW14679	Miraciline. Richar	778	4	100.0	224	20	AAW06931	C. albicans antige
706	4	100.0	191	14	AAW35202	Streptococcus pneu	779	4	100.0	224	21	AAW24829	Arabidopsis thalia
707	4	100.0	191	19	AAW60947	Streptococcus pneu	780	4	100.0	224	21	AAW39745	Arabidopsis thalia
708	4	100.0	191	23	ABW40500	Staphylococcus epi	781	4	100.0	225	21	AAW20264	Arabidopsis thalia
709	4	100.0	192	22	ABW57937	Drosophila melanog	782	4	100.0	225	21	AAW45252	Arabidopsis thalia
710	4	100.0	192	22	AAU20141	Human DNA repair a	783	4	100.0	225	21	AAW50345	Arabidopsis thalia
711	4	100.0	192	22	AAU21794	Novel human neopla	784	4	100.0	225	23	AAU74609	Human WW domain bi
712	4	100.0	195	21	AAW54929	Arabidopsis thalia	785	4	100.0	226	22	ABW24316	Novel human diagno
713	4	100.0	197	21	AAW07817	Amino acid sequenc	786	4	100.0	227	18	AAW09639	Human cytokine, ST
714	4	100.0	197	21	AAW75378	Neisseria meningit	787	4	100.0	227	21	AAW11080	Arabidopsis thalia
715	4	100.0	197	22	ABW09842	Novel human diagno	788	4	100.0	227	21	AAW29316	Arabidopsis thalia
716	4	100.0	198	19	AAW77416	Human GTP binding	789	4	100.0	227	21	AAW39742	Arabidopsis thalia
717	4	100.0	198	21	AAW01281	GTP binding protei	790	4	100.0	227	23	AAU78098	Human T1/ST2 recep
718	4	100.0	198	21	AAW75376	Neisseria gonorrhe	791	4	100.0	227	23	AAU78099	Human T1/ST2 recep
719	4	100.0	198	21	AAW75377	Neisseria meningit	792	4	100.0	228	18	AAW20794	H. pylori transpor
720	4	100.0	198	22	AAU27771	Human full-length	793	4	100.0	229	21	AAW45251	Arabidopsis thalia
721	4	100.0	198	22	AAW74777	Human SAR1 protein	794	4	100.0	229	22	AAW47497	PTPase encoded by
722	4	100.0	198	22	AAW74778	Chinese hamster SA	795	4	100.0	229	23	AAU99941	Dihydrofolate redu
723	4	100.0	198	23	ABW57346	Mouse ischaemic co	796	4	100.0	230	20	AAW00195	Enterococcus faeca
724	4	100.0	199	19	AAW74864	Human secreted pro	797	4	100.0	230	21	AAW91319	Group B Streptococ
725	4	100.0	200	21	AAW45253	Arabidopsis thalia	798	4	100.0	230	23	ABW43414	E faecalis EF097 a
726	4	100.0	201	21	AAW56779	Human prostate can	799	4	100.0	230	23	ABW28247	Streptococcus poly
727	4	100.0	201	22	AAU16430	Human novel secret	800	4	100.0	230	23	ABW28828	Streptococcus poly
728	4	100.0	201	22	AAW74282	Human colon cancer	801	4	100.0	231	23	ABW28829	Putative recombin
729	4	100.0	203	21	AAW16434	Arabidopsis thalia	802	4	100.0	232	22	ABW96506	Streptococcus poly
730	4	100.0	203	23	ABW38851	Staphylococcus epi	803	4	100.0	233	21	AAW24783	Arabidopsis thalia
731	4	100.0	204	21	AAW11891	Arabidopsis thalia	804	4	100.0	233	21	AAW36955	Arabidopsis thalia
732	4	100.0	206	21	AAW15862	Arabidopsis thalia	805	4	100.0	233	23	ABW33643	Lactococcus lactis
733	4	100.0	206	21	AAW21897	Arabidopsis thalia	806	4	100.0	234	21	AAW23163	Arabidopsis thalia
734	4	100.0	206	21	AAW52999	Arabidopsis thalia	807	4	100.0	235	23	AAU74610	Human testicular W
735	4	100.0	207	21	AAW30593	Arabidopsis thalia	808	4	100.0	236	23	AAW37541	Arabidopsis thalia
736	4	100.0	207	21	AAW50581	Arabidopsis thalia	809	4	100.0	236	23	AAU72980	Neisseria meningit
737	4	100.0	208	20	AAW31644	Human transport-as	810	4	100.0	239	21	AAW37540	Arabidopsis thalia
738	4	100.0	208	21	AAW04338	Arabidopsis thalia	811	4	100.0	240	23	ABW41689	Human ovarian anti
739	4	100.0	208	21	AAW60637	Arabidopsis thalia	812	4	100.0	241	21	AAW29981	Arabidopsis thalia
740	4	100.0	208	21	AAW40775	Zea mays protein f	813	4	100.0	244	22	ABW61599	Drosophila melanog

814	4	100.0	244	23	AAU82957	S. cerevisiae B01	887	4	100.0	272	22	ABB61406	Drosophila melanog
815	4	100.0	246	23	ABP60839	Caenorhabditis ele	888	4	100.0	272	22	ABG06359	Novel human diagno
816	4	100.0	247	21	AAAG29960	Arabidopsis thalia	889	4	100.0	272	22	ABG23505	Novel human diagno
817	4	100.0	247	21	AAAG50861	Arabidopsis thalia	890	4	100.0	273	20	AAV35099	Chlamydia pneumoni
818	4	100.0	248	23	ABP26619	Streptococcus poly	891	4	100.0	275	22	AAE13849	Human lung tumour-
819	4	100.0	249	21	AAV56994	C. pneumoniae mfp	892	4	100.0	278	21	AAAG31120	Arabidopsis thalia
820	4	100.0	249	22	ABB60022	Drosophila melanog	893	4	100.0	279	22	AAAB67294	Arabidopsis thalia
821	4	100.0	254	21	AAV83649	HTLV-1 Tax/HLA-A2	894	4	100.0	279	22	AAAV91890	Human immune/haema
822	4	100.0	254	21	AAV56060	HTLV-1 Tax/HLA-A2	895	4	100.0	279	22	AAU19889	Human novel extrac
823	4	100.0	254	21	AAV56084	TCR alpha chain an	896	4	100.0	279	23	ABP48109	Human polypeptide
824	4	100.0	254	21	AAV57660	TCR alpha chain an	897	4	100.0	281	21	AAAG42895	Arabidopsis thalia
825	4	100.0	254	21	AAV57669	Human G-protein co	898	4	100.0	281	22	AAU55502	Propionibacterium
826	4	100.0	254	22	AAE06763	Caspase-8. Uniden	899	4	100.0	281	23	ABG59949	Human DTRP polype
827	4	100.0	254	22	AAAB98656	Novel secreted pro	900	4	100.0	282	21	AAAG14929	Arabidopsis thalia
828	4	100.0	255	23	AAU83190	Human leucine-rich	901	4	100.0	282	21	AAAG30521	Arabidopsis thalia
829	4	100.0	256	19	AAW48300	Staphylococcus aur	902	4	100.0	282	21	AAAG39084	Arabidopsis thalia
830	4	100.0	256	21	AAV70129	Staphylococcus aur	903	4	100.0	282	23	ABP38310	Staphylococcus epi
831	4	100.0	256	22	AAU33732	Staphylococcus aur	904	4	100.0	282	23	ABBA47560	Staphylococcus epi
832	4	100.0	256	22	AAU33732	Staphylococcus aur	905	4	100.0	283	23	ABBA91384	Staphylococcus epi
833	4	100.0	256	22	AAU36942	Staphylococcus aur	906	4	100.0	284	21	AAAG33312	Herbicidally activ
834	4	100.0	256	22	AAU37299	Staphylococcus aur	907	4	100.0	286	19	AAW69247	Zea mays protein f
835	4	100.0	256	22	AAU37888	Staphylococcus aur	908	4	100.0	286	21	AAV56997	Human procaspase 8
836	4	100.0	257	21	AAAB10546	Murine aspartate p	909	4	100.0	286	22	AAE03824	Human gene 7' encod
837	4	100.0	257	21	AAAB10553	Murine aspartate p	910	4	100.0	286	22	AAE03850	Human gene 7' encod
838	4	100.0	257	21	AAAG23162	Arabidopsis thalia	911	4	100.0	286	22	AAAB95427	Human protein sequ
839	4	100.0	257	22	AAE02197	Pig PZP-3. Sus sc	912	4	100.0	286	22	AAAB90727	Human CT585.1 pro
840	4	100.0	258	14	AAAR41004	Partial porcine zo	913	4	100.0	286	22	AAAB88345	Human membrane or
841	4	100.0	258	15	AAAR6951	Serine protease RN	914	4	100.0	286	22	AAAB59578	Human caspase-8.
842	4	100.0	258	15	AAAR55757	Chlamydia pneumoni	915	4	100.0	286	23	ABG64527	Human albumin fusi
843	4	100.0	258	20	AAV35281	C. pneumoniae mfp	916	4	100.0	286	23	ABG64528	Human albumin fusi
844	4	100.0	258	21	AAV56993	Novel human diagno	917	4	100.0	286	23	ABP38214	Streptococcus epi
845	4	100.0	258	22	ABG21800	Novel human diagno	918	4	100.0	286	23	ABP30472	Streptococcus poly
846	4	100.0	258	22	ABG24313	C. pneumoniae BVH-	919	4	100.0	287	20	AAV01403	Secreted protein e
847	4	100.0	258	23	ABP61993	Chlamydia pneumoni	920	4	100.0	287	23	ABAB57151	Mouse ischaemic co
848	4	100.0	258	23	ABAB90553	Streptococcus poly	921	4	100.0	287	23	ABBA48469	Listeria monocytog
849	4	100.0	258	23	ABP29565	Streptococcus epi	922	4	100.0	288	22	ABAB68032	Drosophila melanog
850	4	100.0	260	23	ABP39164	Aspen homeobox pro	923	4	100.0	288	22	ABG25553	Novel human diagno
851	4	100.0	261	20	AAV32096	Arabidopsis thalia	924	4	100.0	289	21	AAAG24512	Arabidopsis thalia
852	4	100.0	261	21	AAAG31121	Novel human diagno	925	4	100.0	291	22	AAAM39455	Human polypeptide
853	4	100.0	261	22	ABG15695	Novel human diagno	926	4	100.0	292	22	AAAB95755	Human protein sequ
854	4	100.0	261	23	ABAB54690	Lactococcus lactis	927	4	100.0	295	20	AAV34650	Chlamydia pneumoni
855	4	100.0	262	17	AAAR9726	B10 single chain T	928	4	100.0	298	22	AAU01247	B. subtilis Ketopa
856	4	100.0	262	23	ABBA8921	Listeria monocytog	929	4	100.0	298	23	AAW47997	Human RNA helicase
857	4	100.0	264	10	AAAP90497	Protein sequence i	930	4	100.0	299	21	AAAB08915	Human secreted pro
858	4	100.0	264	10	AAAP90609	Sequence of amy 37	931	4	100.0	299	23	ABBT7630	AMPV serine/threo
859	4	100.0	264	21	AAAG05410	Arabidopsis thalia	932	4	100.0	299	23	ABBT7933	Streptococcus poly
860	4	100.0	265	21	AAAG42941	Arabidopsis thalia	933	4	100.0	299	23	ABBA31890	Herbicidally activ
861	4	100.0	265	21	AAAG30522	Arabidopsis thalia	934	4	100.0	301	22	ABBI0998	Human secreted pro
862	4	100.0	265	21	AAAG37539	Arabidopsis thalia	935	4	100.0	301	23	AAU97911	Human olfactory an
863	4	100.0	265	21	AAAG39085	Arabidopsis thalia	936	4	100.0	301	23	AAU95787	Human 63497 protei
864	4	100.0	266	18	AAW11896	MACH isoform alpha	937	4	100.0	302	21	AAAG46712	Arabidopsis thalia
865	4	100.0	266	21	AAAG21996	Arabidopsis thalia	938	4	100.0	302	23	AAU79333	Novel human vomero
866	4	100.0	266	21	AAAG53260	Arabidopsis thalia	939	4	100.0	306	22	ABG25552	Novel human diagno
867	4	100.0	267	21	AAAG14931	Arabidopsis thalia	940	4	100.0	307	22	ABAB67832	Drosophila melanog
868	4	100.0	267	21	AAAG33313	Zea mays protein f	941	4	100.0	308	22	AAAB91019	Human immune/haema
869	4	100.0	267	21	AAAG42897	Arabidopsis thalia	942	4	100.0	308	22	AAAB87771	Human T2R41 amino
870	4	100.0	267	22	AAW79578	Human protein SEO	943	4	100.0	308	22	AAU19888	Human novel extrac
871	4	100.0	268	15	AAAR47857	Streptococcal fibr	944	4	100.0	308	22	AAU19888	Human novel extrac
872	4	100.0	268	21	AAAG20263	Arabidopsis thalia	945	4	100.0	308	23	ABP48003	Human polypeptide
873	4	100.0	268	21	AAAG50344	Arabidopsis thalia	946	4	100.0	308	23	ABP48108	Human polypeptide
874	4	100.0	268	22	ABBI1752	Human globulactoma	947	4	100.0	310	23	ABP27917	Streptococcus poly
875	4	100.0	269	19	AAV85990	S. pneumoniae deri	948	4	100.0	311	19	AAW42641	Protein sequence t
876	4	100.0	269	22	AAAB96192	Putative P. abysal	949	4	100.0	311	21	AAAG21031	Arabidopsis thalia
877	4	100.0	269	22	AAW41988	Human polypeptide	950	4	100.0	312	21	AAAG05409	Arabidopsis thalia
878	4	100.0	270	19	ABP55094	Streptococcus pneu	951	4	100.0	312	21	AAAG42940	Arabidopsis thalia
879	4	100.0	270	23	ABP54588	S. pneumoniae SP04	952	4	100.0	312	21	AAAG50418	Arabidopsis thalia
880	4	100.0	271	18	AAW20780	H. pylori transport	953	4	100.0	313	22	AAAG69455	Human purified sec
881	4	100.0	271	20	AAW89032	Polypeptide fragme	954	4	100.0	313	18	AAW21640	Grepevine leafroll
882	4	100.0	271	21	AAAG14930	Arabidopsis thalia	955	4	100.0	313	20	AAV25719	Human secreted pro
883	4	100.0	271	21	AAAG42896	Arabidopsis thalia	956	4	100.0	313	23	ABBO6630	G protein-coupled
884	4	100.0	271	22	ABAB51150	Human secreted pro	957	4	100.0	314	22	ABG12293	Novel human diagno
885	4	100.0	271	22	ABAB82031	S. epidermidis thali	958	4	100.0	315	21	AAAG31119	Arabidopsis thalia
886	4	100.0	272	19	AAW36111	Mouse T-cell recep	959	4	100.0	316	23	ABBO6639	G protein-coupled

960 4 100.0 319 21 AAG39083 Arabidopsis thalia  
 961 4 100.0 319 22 AAU24610 Human olfactory re  
 962 4 100.0 319 23 AAG71745 Human olfactory re  
 963 4 100.0 319 23 AAU95527 Human olfactory an  
 964 4 100.0 319 23 AB066638 G protein-coupled  
 965 4 100.0 319 23 AU085230 G-coupled olfactor  
 966 4 100.0 320 21 AAG30520 Arabidopsis thalia  
 967 4 100.0 321 21 AAG33311 Zea mays protein f  
 968 4 100.0 321 22 ABB68664 Drosophila melanog  
 969 4 100.0 321 22 AAM40202 Human polypeptide  
 970 4 100.0 321 23 ABB49351 Murine monocytog  
 971 4 100.0 322 21 AAY75963 Murine skin cell p  
 972 4 100.0 322 22 AAB55902 Skin cell protein,  
 973 4 100.0 322 23 ABB72102 Murine protein iso  
 974 4 100.0 323 22 AAM41241 Human polypeptide  
 975 4 100.0 324 22 ABB11401 Human acrosomal pr  
 976 4 100.0 326 19 AAW44194 Arabidopsis G prot  
 977 4 100.0 326 20 AAY19805 B. burgdorferi ant  
 978 4 100.0 326 21 AAG35727 Arabidopsis thalia  
 979 4 100.0 326 22 ABB11609 Human secreted pro  
 980 4 100.0 326 23 ABB31281 Herbicidally activ  
 981 4 100.0 327 20 AAY25157 Maize tryptophan s  
 982 4 100.0 329 21 AAB51794 Gene 2l human secr  
 983 4 100.0 329 21 AAG33171 Arabidopsis thalia  
 984 4 100.0 329 21 AAG50417 Arabidopsis thalia  
 985 4 100.0 331 21 AAG05052 Arabidopsis thalia  
 986 4 100.0 331 22 AAM50916 Propionibacterium  
 987 4 100.0 331 23 AAM52838 Physcomitrella pat  
 988 4 100.0 333 21 AAG18622 Arabidopsis thalia  
 989 4 100.0 333 21 AAY95355 Arabidopsis wax sy  
 990 4 100.0 333 22 ABB58362 Drosophila melanog  
 991 4 100.0 333 23 ABB33824 Herbicidally activ  
 992 4 100.0 335 14 AAR34539 M protein of atten  
 993 4 100.0 335 21 AAY57604 Human protein SEQ  
 994 4 100.0 335 22 AAG06645 Novel human diagno  
 995 4 100.0 336 19 AAW69427 Human secreted pro  
 996 4 100.0 336 20 AAM88330 Mannosyl transfera  
 997 4 100.0 337 22 AAM25693 Human protein sequ  
 998 4 100.0 337 23 ABA41673 Human ovarian anti  
 999 4 100.0 338 20 AAW87689 Human H<sup>+</sup>FT19 poly  
 1000 4 100.0 339 21 AAG35122 Arabidopsis thalia

ALIGNMENTS

RESULT 1  
 ID AAW45956 standard; peptide; 4 AA.  
 AC AAW45956;

DT 30-JUN-1998 (first entry)

DE Amyloid beta peptide fragment.

KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.

OS Homo sapiens.

PN WO9721728-A1. ✓

PD 19-JUN-1997.

PF 09-DEC-1996; 96WO-SE01621.

PR 29-DEC-1995; 95US-0009386.

PR 12-DEC-1995; 95SE-0004467.

PA (KARO-) KAROLINSKA INNOVATIONS AB.

PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

XX WPI; 1997-332723/30.  
 XX Use of new and known peptide(s) for inhibition of polymerisation of  
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
 PT Down's syndrome associated with amyloidosis.  
 XX Example 1; Figure 2B; 31pp; English.  
 XX This sequence represents a fragment of the amyloid beta peptide. The  
 CC invention relates to the use of peptide compounds for inhibition of  
 CC polymerisation of amyloid beta peptide (ABP), as model substances for  
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a  
 CC tool for the identification of other organic compounds with similar  
 CC functional properties, or as ligands in positron emission tomography.  
 CC The peptides may be used in treatment of amyloidosis, especially in  
 CC treatment of Alzheimer's disease associated with amyloidosis, for  
 CC treatment or prevention of demens in patients with Down's syndrome, for  
 CC treatment or prevention of hereditary cerebral haemorrhage with  
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of  
 CC human amyloid protein. They can also be used for identifying other  
 CC molecules with similar properties and/or as ligands for detection of  
 CC amyloid deposits using e.g. positron emission tomography.  
 XX Sequence 4 AA;  
 SQ  
 QY 1 KLVP 4  
 DB 1 KLVP 4  
 Query Match 100.0%; Score 4; DB 18; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 AAY79936  
 ID AAY79936 standard; peptide; 4 AA.  
 AC AAY79936;  
 DT 11-MAY-2000 (first entry)  
 DE Beta-amyloid recognition peptide SEQ ID NO:1.  
 DE Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;  
 KW Alzheimer's disease; neuroprotective; nontropic.  
 OS Homo sapiens.  
 PN US6022859-A. ✓  
 PD 08-FEB-2000.  
 PF 14-NOV-1997; 97US-0970833.  
 PR 15-NOV-1996; 96US-0030840.  
 PR (WISC ) WISCONSIN ALUMNI RES FOUND.  
 PA Murphy RM, Kiessling LL;  
 PI WPI; 2000-160387/14.  
 PT Beta-amyloid inhibitor useful for treating Alzheimer's disease -  
 PS Example; Column 7; 15pp; English.  
 XX The present invention describes a beta-amyloid inhibitor peptide.  
 CC Beta-amyloid inhibitors have neuroprotective and nontropic  
 CC properties. The inhibitor peptides are useful for the treatment of  
 CC Alzheimer's disease. The present sequence represents a beta-amyloid  
 CC recognition peptide used in the exemplification of present invention.

```

XX SQ Sequence 4 AA;
CC Query Match 100.0%; Score 4; DB 21; Length 4;
CC Best Local Similarity 100.0%; Pred. No. 7.8e+05;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVF 4
DB 1 KLVF 4

RESULT 3
AAB82627 standard; Peptide; 4 AA.
XX AAB82627;
XX
XX 02-OCT-2001 (first entry)
XX
XX All-D peptide used in Alzheimer's disease vaccine.
XX
XX Alzheimer's disease; amyloidosis; amyloid-related disease;
XX vaccine; therapy; antigen.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH MISC-difference 1..4
XX FT MISC-difference /note="all D-form residues"
XX
XX PN MO200139796-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 29-NOV-2000; 2000MO-CA01413.
XX
XX PR 29-NOV-1999; 99US-0168594.
XX
XX PR 28-NOV-2000; 2000US-0724842.
XX
XX PA (NEUR-) NEUROCHEM INC.
XX
XX PI Chalfour R, Hebert L, Kong X, Gervais F;
XX
XX DR MPI; 2001-441458/47.
XX
XX PT Preventing/creating amyloid-related disease, especially Alzheimer's
XX PT disease, comprises administering antigenic all-D peptide, e.g. as
XX PT vaccine, which elicits production of antibodies to prevent
XX PT fibrillogenesis and associated cellular toxicity -
XX PT
XX PS Disclosure; Page 11; 31pp; English.
XX
XX CC The present sequence is that of an all-D peptide suitable for
XX CC use for preparing vaccines for preventing or treating Alzheimer's
XX CC disease and other amyloid related disorders in humans. It is based
XX CC on a portion of amyloid-beta peptide (see AAB82622), and may be
XX CC modified by removing or inserting 1 or more amino acid residues, or
XX CC by substituting 1 or more amino acid residues with other amino acid
XX CC residues or non-amino acid fragments. Vaccines of the invention
XX CC are produced using 'non-self' peptides synthesised from the
XX CC unnatural D-configuration amino acids to avoid the drawbacks of
XX CC 'self' proteins. The all-D peptides need not be aggregated to be
XX CC operative or immunogenic. They preferably interact with at
XX CC least 1 region of an amyloid protein, e.g. the beta-sheet region
XX CC or GAG-binding site region, the amyloid-beta peptide, or their
XX CC immunogenic fragments, protein conjugates, immunogenic derivative
XX CC peptides and immunogenic peptidomimetics. Examples include all-D
XX CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
XX CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
XX CC derivative peptides given in AAB82623-64. The vaccine elicits a
XX CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
XX CC associated cellular toxicity. The amyloid related diseases may be

```

```

CC localised amyloidosis, e.g. diabetes type II, neurodegenerative
CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
CC related disorders, or systemic amyloidosis associated with chronic
CC infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
CC systemic amyloidosis found in long-term haemodialysis patients.
XX
XX SQ Sequence 4 AA;
CC Query Match 100.0%; Score 4; DB 22; Length 4;
CC Best Local Similarity 100.0%; Pred. No. 7.8e+05;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVF 4
DB 1 KLVF 4

RESULT 4
AAB82635 standard; Peptide; 4 AA.
XX AAB82635;
XX
XX 02-OCT-2001 (first entry)
XX
XX All-D peptide used in Alzheimer's disease vaccine.
XX
XX Alzheimer's disease; amyloidosis; amyloid-related disease;
XX vaccine; therapy; antigen.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH MISC-difference 1..4
XX FT MISC-difference /note="all D-form residues"
XX FT Modified-site 6
XX FT FT /note="C-terminal amide"
XX
XX PN MO200139796-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 29-NOV-2000; 2000MO-CA01413.
XX
XX PR 29-NOV-1999; 99US-0168594.
XX
XX PR 28-NOV-2000; 2000US-0724842.
XX
XX PA (NEUR-) NEUROCHEM INC.
XX
XX PI Chalfour R, Hebert L, Kong X, Gervais F;
XX
XX DR MPI; 2001-441458/47.
XX
XX PT Preventing/creating amyloid-related disease, especially Alzheimer's
XX PT disease, comprises administering antigenic all-D peptide, e.g. as
XX PT vaccine, which elicits production of antibodies to prevent
XX PT fibrillogenesis and associated cellular toxicity -
XX PT
XX PS Disclosure; Page 11; 31pp; English.
XX
XX CC The present sequence is that of an all-D peptide suitable for
XX CC use in preparing vaccines for preventing or treating Alzheimer's
XX CC disease and other amyloid related disorders in humans. It is based
XX CC on a portion of amyloid-beta peptide (see AAB82622), and may be
XX CC modified by removing or inserting 1 or more amino acid residues, or
XX CC by substituting 1 or more amino acid residues with other amino acid
XX CC residues or non-amino acid fragments. Vaccines of the invention
XX CC are produced using 'non-self' peptides synthesised from the
XX CC unnatural D-configuration amino acids to avoid the drawbacks of
XX CC 'self' proteins. The all-D peptides need not be aggregated to be
XX CC operative or immunogenic. They preferably interact with at

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CC least 1 region of an amyloid protein, e.g. the beta-sheet region  
 CC or GAG-binding site region, the amyloid-beta peptide, or their  
 CC immunogenic fragments, protein conjugates, immunogenic derivative  
 CC peptides and immunogenic peptidomimetics. Examples include all-D  
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,  
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D  
 CC derivative peptides given in AAB82623-64. The vaccine elicits a  
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and  
 CC associated cellular toxicity. The amyloid related diseases may be  
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative  
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob  
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein  
 CC related disorders, or systemic amyloidosis associated with chronic  
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and  
 CC systemic amyloidosis found in long-term haemodialysis patients.

XX Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 1 KLVF 4

RESULT 5  
 AAB48479  
 ID AAB48479 standard; Peptide; 4 AA.

XX AC AAB48479;

XX DT 02-MAR-2001 (first entry)

XX DE Antifibrillogenic peptide #6.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200068263-A2.

XX PD 16-NOV-2000.

XX PF 04-MAY-2000; 2000WO-CA00515.

XX PR 05-MAY-1999; 99US-0132592.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Chalifour R, Gervais F, Gupta A;

XX PS WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic -

XX PS Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are  
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's  
 CC disease. Peptides AAB48474-B48496 were identified from the  
 CC glycosaminoglycan binding region and the prot-prot interaction region of  
 CC the human amyloid protein.

XX Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 1 KLVF 4

RESULT 6  
 AAB48487  
 ID AAB48487 standard; Peptide; 4 AA.

XX AC AAB48487;

XX DT 02-MAR-2001 (first entry)

XX DE Antifibrillogenic peptide #14.

XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 4 /note= "C-terminal amide"

XX PN WO200068263-A2.

XX PD 16-NOV-2000.

XX PF 04-MAY-2000; 2000WO-CA00515.

XX PR 05-MAY-1999; 99US-0132592.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Chalifour R, Gervais F, Gupta A;

XX PS WPI; 2001-031852/04.

XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic -

XX PS Claim 7; Page 25; 46pp; English.

XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are  
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's  
 CC disease. Peptides AAB48474-B48496 were identified from the  
 CC glycosaminoglycan binding region and the prot-prot interaction region of  
 CC the human amyloid protein.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 1 KLVF 4

RESULT 7  
 AAU96815  
 ID AAU96815 standard; peptide; 4 AA.

XX

AAU96815;  
30-JUL-2002 (first entry)  
Amyloid targeting peptide #5.  
Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD; transmissible cerebral amyloidosis; transmissible virus dementia; scrapie; transmissible mink encephalopathy; BSE; type II diabetes; bovine spongiform encephalopathy; inflammation associated amyloid; primary amyloidosis; feline spongiform encephalopathy; Alzheimer's disease; prion-mediated disease; blood-brain barrier; dialysis-related amyloidosis; light chain-related amyloidosis; cerebral amyloid angiopathy.  
Synthetic.  
Key Location/Qualifiers  
FT Misc-difference 1..4 /note= "Preferably D-form residue"  
FT WO200207781-A2.  
PD 31-JAN-2002.  
PD 25-JUL-2001; 2001WO-CA01071.  
PF 25-JUL-2000; 2000US-220808P.  
PR 24-JUL-2001; 2001US-0915092.  
XX (NEUR-) NEUROCHEM INC.  
XX Gervais F, Kong X, Chalfour R, Migneault D;  
XX MPI; 2002-371447/40.  
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
XX plaques and/or for the treatment of amyloidosis disorders -  
XX Claim 49; Page 21; 57pp; English.  
XX The invention relates to an amyloid-targeting imaging agent comprising  
XX an amyloid targeting moiety, a linker moiety and a labelling moiety.  
XX The agent is of general formula A-C-(A<sub>1</sub>n<sub>1</sub>k)-z-A<sub>1</sub>a<sub>1</sub>b (I) where  
XX z = 0 - 1; A<sub>1</sub>t = an amyloid targeting moiety; A<sub>1</sub>n<sub>1</sub>k = a linker  
XX moiety; and A<sub>1</sub>a<sub>1</sub>b = a labelling moiety. Also included are imaging  
XX amyloid deposition or diagnosing an amyloid-related condition in a  
XX patient involving administering (I) to the patient, and ultrasound  
XX imaging (I) in the patient to determine the presence of amyloid or  
XX amyloid-related condition; and a kit for preparing a radiopharmaceutical  
XX preparation comprising (I), a reducing agent, a buffering agent, a  
XX trachealating agent, and instructions for the preparation and use of the  
XX radiopharmaceutical in the imaging of amyloid or an amyloid-related  
XX condition. The agents are used for imaging amyloid deposition and for  
XX diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease  
XX (CJD), Kuru, transmissible cerebral amyloidosis (transmissible virus  
XX dementia), familial CJD, scrapie, transmissible mink encephalopathy,  
XX bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
XX type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
XX non-transmissible cerebral amyloidosis, Alzheimer's disease,  
XX prion-mediated diseases, dialysis-related amyloidosis, light  
XX chain-related amyloidosis, cerebral amyloid angiopathy. The agents are  
XX capable of crossing the blood-brain barrier and are capable of binding  
XX specifically to amyloid plaques. The present sequence is a peptide  
XX forming the amyloid targeting moiety of the agent of the invention.  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 4; DB 23; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4

Db 1 KLVF 4  
||||  
RESULT 8  
AAU96823  
ID AAU96823 standard; peptide; 4 AA.  
XX  
XX AAU96823;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX Amyloid targeting peptide #13.  
XX  
XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
XX transmissible cerebral amyloidosis; transmissible virus dementia;  
XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
XX bovine spongiform encephalopathy; inflammation associated amyloid;  
XX primary amyloidosis; feline spongiform encephalopathy;  
XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
XX dialysis-related amyloidosis; light chain-related amyloidosis;  
XX cerebral amyloid angiopathy.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX FT Misc-difference 1..4 /note= "Preferably D-form residue"  
XX FT Modified-site 4/note= "Phe is amidated"  
XX FT WO200207781-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 25-JUL-2001; 2001WO-CA01071.  
XX  
XX 25-JUL-2000; 2000US-220808P.  
XX  
XX 24-JUL-2001; 2001US-0915092.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Gervais F, Kong X, Chalfour R, Migneault D;  
XX MPI; 2002-371447/40.  
XX  
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
XX plaques and/or for the treatment of amyloidosis disorders -  
XX Claim 49; Page 21; 57pp; English.  
XX  
XX The invention relates to an amyloid-targeting imaging agent comprising  
XX an amyloid targeting moiety, a linker moiety and a labelling moiety.  
XX The agent is of general formula A-C-(A<sub>1</sub>n<sub>1</sub>k)-z-A<sub>1</sub>a<sub>1</sub>b (I) where  
XX z = 0 - 1; A<sub>1</sub>t = an amyloid targeting moiety; A<sub>1</sub>n<sub>1</sub>k = a linker  
XX moiety; and A<sub>1</sub>a<sub>1</sub>b = a labelling moiety. Also included are imaging  
XX amyloid deposition or diagnosing an amyloid-related condition in a  
XX patient involving administering (I) to the patient, and ultrasound  
XX imaging (I) in the patient to determine the presence of amyloid or  
XX amyloid-related condition; and a kit for preparing a radiopharmaceutical  
XX preparation comprising (I), a reducing agent, a buffering agent, a  
XX trachealating agent, and instructions for the preparation and use of the  
XX radiopharmaceutical in the imaging of amyloid or an amyloid-related  
XX condition. The agents are used for imaging amyloid deposition and for  
XX diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease  
XX (CJD), Kuru, transmissible cerebral amyloidosis (transmissible virus  
XX dementia), familial CJD, scrapie, transmissible mink encephalopathy,  
XX bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
XX type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
XX non-transmissible cerebral amyloidosis, Alzheimer's disease,  
XX prion-mediated diseases, dialysis-related amyloidosis, light  
XX chain-related amyloidosis, cerebral amyloid angiopathy. The agents are  
XX capable of crossing the blood-brain barrier and are capable of binding

CC specifically to amyloid plaques. The present sequence is a peptide  
 CC forming the amyloid targeting moiety of the agent of the invention.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 4; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 Db 1 KLVF 4  
 RESULT 9  
 AAU11653  
 ID AAU11653 standard; Peptide; 4 AA.  
 XX  
 AC AAU11653;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Peptide #6, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 XX  
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200185093-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 22-DEC-2000; 2000WO-IB02078.  
 XX  
 PR 23-DEC-1999; 99US-171877P.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 PI Green AM, Gervais F;  
 XX  
 DR WPI; 2002-075222/10.  
 XX  
 PT Inhibiting cerebral amyloid angiopathy used for treating e.g.  
 PT Alzheimer's disease comprises contacting blood vessel wall cell with  
 PT amyloid-beta 40 inhibitor -  
 XX  
 PS Disclosure; Page 10; 68pp; English.  
 XX  
 CC The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting  
 CC a blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral  
 CC amyloid angiopathy, particularly Alzheimer's disease, hereditary  
 CC cerebral haemorrhage with amyloidosis of the Dutch type and  
 CC haemorrhagic stroke. The present sequence represents one of a group  
 CC of peptides (AAU11648-AAU11669, AAU11910 & AAU11911) that were used in  
 CC the invention as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 CC The Abeta40 inhibitor was used in the invention to treat a disease  
 CC state characterised by cerebral amyloid angiopathy (CAA).  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 4; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 Db 1 KLVF 4

RESULT 10  
 AAU11661  
 ID AAU11661 standard; Peptide; 4 AA.  
 XX  
 AC AAU11661;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Peptide #14, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 XX  
 KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "C-terminal amide"  
 XX  
 PN WO200185093-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 22-DEC-2000; 2000WO-IB02078.  
 XX  
 PR 23-DEC-1999; 99US-171877P.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 PI Green AM, Gervais F;  
 XX  
 DR WPI; 2002-075222/10.  
 XX  
 PT Inhibiting cerebral amyloid angiopathy used for treating e.g.  
 PT Alzheimer's disease comprises contacting blood vessel wall cell with  
 PT amyloid-beta 40 inhibitor -  
 XX  
 PS Disclosure; Page 10; 68pp; English.  
 XX  
 CC The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting  
 CC a blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral  
 CC amyloid angiopathy, particularly Alzheimer's disease, hereditary  
 CC cerebral haemorrhage with amyloidosis of the Dutch type and  
 CC haemorrhagic stroke. The present sequence represents one of a group  
 CC of peptides (AAU11648-AAU11669, AAU11910 & AAU11911) that were used in  
 CC the invention as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 CC The Abeta40 inhibitor was used in the invention to treat a disease  
 CC state characterised by cerebral amyloid angiopathy (CAA).  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 4; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 Db 1 KLVF 4  
 RESULT 11  
 AAR87922  
 ID AAR87922 standard; peptide; 5 AA.  
 XX  
 AC AAR87922;  
 XX  
 DT 01-MAR-1996 (first entry)  
 XX  
 DE Test peptide used in study of antagonism of amyloid beta protein.  
 XX



KW amnesia; amyloid beta; Alzheimer's disease.  
 XX Synthetic.  
 OS  
 PN WO9508999-A1.  
 XX  
 PD 06-APR-1995.  
 XX  
 PF 16-SEP-1994; 94WO-US10475.  
 XX  
 PR 29-SEP-1993; 93US-0127904.  
 XX  
 PA (CITY ) CITY OF HOPE.  
 XX  
 PI Roberts E;  
 PS  
 DR WPI; 1995-147244/19.  
 XX  
 PT New peptide(s) which block binding of amyloid beta protein - used  
 for antagonising the amnesic effects of amyloid beta protein,  
 PT partic. in Alzheimer's disease  
 XX  
 PS Disclosure; Page 9; 27pp; English.  
 XX  
 CC The invention relates to three new peptides which block the amnesic  
 effects of amyloid beta protein and which can be used to ameliorate  
 CC amnesia and other neurotoxicity in Alzheimer's disease caused by  
 CC deposition of this protein. The peptides themselves are not amnesic or  
 CC memory-enhancing. The new peptides are described in AAR87912, AAR87913  
 CC and AAR87914.  
 CC The present sequence is an additional peptide tested in the process  
 CC but found not to be active.  
 CC  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 4; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 1 KLVF 4  
 RESULT 12  
 AAW02315  
 ID AAW02315 standard; peptide; 5 AA.  
 XX  
 AC AAW02315;  
 XX  
 DT 02-MAY-1997 (first entry)  
 XX  
 DE Beta-amyloid modulator peptide #6.  
 XX  
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9628471-A1.  
 XX  
 PD 19-SEP-1996.  
 XX  
 PF 14-MAR-1996; 96WO-US03492.  
 XX  
 PR 27-OCT-1995; 95US-0548998.  
 PR 14-MAR-1995; 95US-0404831.  
 PR 07-JUN-1995; 95US-0475579.

XX  
 PA (PHAR-) PHARM PEPTIDES INC.  
 XX  
 PI Benjamin H, Chin J, Finkel MA, Garnick MB, Gelfer ML;  
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
 PI Molineaux S, Musso G, Reed MO, Signer ER, Wakefield J;  
 XX  
 DR WPI; 1996-433762/43.  
 XX  
 PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
 PT protein coupled (in)directly to at least 1 modifying gp., useful in  
 PT treatment of Alzheimer's disease  
 XX  
 PS Claim 16; Page 91; 106pp; English.  
 XX  
 CC AAW02310-W02332 represent the peptide portions of the beta-amyloid  
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
 CC kilodalton peptide that is the major protein component of amyloid  
 CC plaques. Amyloid plaques are present both in the brain lesions, and in  
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.  
 CC The amyloid modulators of the invention comprise an amyloidogenic protein  
 CC or peptide (such as this sequence) coupled directly or indirectly to at  
 CC least one modifying group. The modifying group is preferably a cyclic,  
 CC heterocyclic, or polycyclic group, such as decalin, a cholan1 group, a  
 CC biotin containing group, or a fluorescein containing group. These  
 CC compounds then modulate the aggregation of these sequences to natural  
 CC amyloid proteins or peptides when contacted with the natural  
 CC amyloidogenic proteins or peptides. The modulator compounds can be used  
 CC in the treatment of disorders associated with amyloidosis, such as  
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,  
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
 CC and other types of amyloidosis. The modulators are also useful for the  
 CC treatment of disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease.  
 CC  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 4; DB 17; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 1 KLVF 4  
 RESULT 13  
 AAW45933  
 ID AAW45933 standard; peptide; 5 AA.  
 XX  
 AC AAW45933;  
 XX  
 DT 08-JUL-1998 (first entry)  
 XX  
 DE Partial sequence of amyloid beta peptide critical for its polymerisation.  
 XX  
 KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9721728-A1.  
 XX  
 PD 19-JUN-1997.  
 XX  
 PF 09-DEC-1996; 96WO-SR01621.  
 XX  
 PR 29-DEC-1995; 95US-0009386.  
 PR 12-DEC-1995; 95SE-0004467.

```

PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX WPI; 1997-332723/30.
XX Use of new and known peptide(s) for inhibition of polymerisation of
XX amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
XX Down's syndrome associated with amyloidosis.
XX Example 5; Page 14; 31pp; English.
XX This is a partial sequence of the amyloid beta peptide which is critical
XX for its polymerisation. The invention relates to the use of peptide
XX compounds for inhibition of polymerisation of amyloid beta peptide
XX (ABP), as model substances for synthesis of ABP-ligands for inhibition
XX of polymerisation of ABP, as a tool for the identification of other
XX organic compounds with similar functional properties, or as ligands in
XX positron emission tomography. The peptides may be used in treatment of
XX amyloidosis, especially in treatment of Alzheimer's disease associated
XX with amyloidosis, for treatment or prevention of demens in patients with
XX Down's syndrome, for treatment or prevention of hereditary cerebral
XX haemorrhage with amyloidosis (Dutch type) or for the prevention of
XX fibril formation of human amyloid protein. They can also be used for
XX identifying other molecules with similar properties and/or as ligands
XX for detection of amyloid deposits using e.g. positron emission
XX tomography.
XX Sequence 5 AA;
XX Query Match 100.0%; Score 4; DB 18; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVF 4
Db 1 KLVF 4
XX
XX RESULT 14
XX AAW45950
XX ID AAW45950 standard; peptide; 5 AA.
XX AC AAW45950;
XX 30-JUN-1998 (first entry)
XX Amyloid beta peptide fragment.
XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
XX positron emission tomography; PET; Down's syndrome; amyloidosis.
XX Homo sapiens.
XX WO9721728-A1.
XX 19-JUN-1997.
XX 09-DEC-1996; 96WO-SE01621.
XX 29-DEC-1995; 95US-0009386.
XX 12-DEC-1995; 95SE-0004467.
XX (KARO-) KAROLINSKA INNOVATIONS AB.
XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX WPI; 1997-332723/30.
XX Use of new and known peptide(s) for inhibition of polymerisation of
XX amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
XX Down's syndrome associated with amyloidosis.
XX Example 5; Page 14; 31pp; English.
XX Sequences AAW45962-6 represent a fragment of the amyloid beta peptide
XX KLVFF with an amino acid residue replaced with alanine. The invention
XX relates to the use of peptide compounds for inhibition of polymerisation
XX of amyloid beta peptide (ABP), as model substances for synthesis of
XX ABP-ligands for inhibition of polymerisation of ABP, as a tool for the
XX identification of other organic compounds with similar functional
XX properties, or as ligands in positron emission tomography. The peptides
XX may be used in treatment of amyloidosis, especially in treatment of
XX
XX Query Match 100.0%; Score 4; DB 18; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVF 4
Db 2 KLVF 5
XX
XX RESULT 15
XX AAW45966
XX ID AAW45966 standard; peptide; 5 AA.
XX AC AAW45966;
XX 30-JUN-1998 (first entry)
XX Peptide derived from amyloid beta peptide fragment.
XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
XX positron emission tomography; PET; Down's syndrome; amyloidosis.
XX Homo sapiens.
XX Synthetic.
XX WO9721728-A1.
XX 19-JUN-1997.
XX 09-DEC-1996; 96WO-SE01621.
XX 29-DEC-1995; 95US-0009386.
XX 12-DEC-1995; 95SE-0004467.
XX (KARO-) KAROLINSKA INNOVATIONS AB.
XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX WPI; 1997-332723/30.
XX Use of new and known peptide(s) for inhibition of polymerisation of
XX amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
XX Down's syndrome associated with amyloidosis.
XX Example 1; Figure 2C; 31pp; English.
XX Sequences AAW45962-6 represent a fragment of the amyloid beta peptide
XX KLVFF with an amino acid residue replaced with alanine. The invention
XX relates to the use of peptide compounds for inhibition of polymerisation
XX of amyloid beta peptide (ABP), as model substances for synthesis of
XX ABP-ligands for inhibition of polymerisation of ABP, as a tool for the
XX identification of other organic compounds with similar functional
XX properties, or as ligands in positron emission tomography. The peptides
XX may be used in treatment of amyloidosis, especially in treatment of

```

CC Alzheimer's disease associated with amyloidosis, for treatment or  
 CC prevention of demens in patients with Down's syndrome, for treatment or  
 CC prevention of hereditary cerebral haemorrhage with amyloidosis (Dutch  
 CC type) or for the prevention of fibril formation of human amyloid  
 CC protein. They can also be used for identifying other molecules with  
 CC similar properties and/or as ligands for detection of amyloid deposits  
 CC using e.g. positron emission tomography.

XX Sequence 5 AA;

Query Match 100.0%; Score 4; DB 18; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Gaps 0;

QY 1 KLVF 4  
 1 KLVF 4

Db 1 KLVF 4

RESULT 16

AAW29089 standard; peptide; 5 AA.

AC AAW29089;

DT 20-JUL-1999 (first entry)

DE A-beta-binding peptide fragment conjugated to cyclosporin.

KW Cyclosporin; A-beta peptide; conjugate; neurological disease;

KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;

KW ALS; non-immunosuppressive; amyloid plaque formation.

OS Homo sapiens.

XX Location/Qualifiers

FT Modified-site 5 /note= "The C-terminal is condensed onto the side

PN MO910374-A1.

PD 04-MAR-1999.

PF 25-AUG-1998; 98MO-US17544.

PR 26-AUG-1997; 97US-0057751.

PA (WISC ) WISCONSIN ALUMNI RES FOUND.

PI Rich DH, Solomon ME;

DR WPI; 1999-276928/23.

PT New A-beta-binding peptide conjugates and Csa analogs - useful in  
 PT treatment of neurological diseases e.g. Alzheimer's disease,  
 PT multiple sclerosis etc.

PS Claim 5; Page 98; 129pp; English.

CC New conjugates are disclosed which are of formula A-2, in which: A is  
 CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506  
 CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more  
 CC contiguous residues of A-beta peptide. The compounds are novel chemical  
 CC inducers of dimerization which are non-immunosuppressive and which are  
 CC inhibitors of A-beta peptide aggregation and deposition in amyloid  
 CC plaques. The adverse consequences of amyloid plaque formation can be  
 CC prevented or ameliorated by sequestering the A-beta to cyclophilin or FKBP,  
 CC form with a conjugate which links the A-beta to cyclophilin or FKBP,  
 CC therefore providing a mechanism to minimize the amount of free A-beta  
 CC available for fibril formation and deposition. The compounds can be used  
 CC for the treatment of Alzheimer's disease, multiple sclerosis and

CC amyotrophic lateral sclerosis.

XX Sequence 5 AA;

Query Match 100.0%; Score 4; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Gaps 0;

QY 1 KLVF 4  
 1 KLVF 4

Db 1 KLVF 4

RESULT 17

AAW89367 standard; peptide; 5 AA.

AC AAW89367;

DT 02-MAR-1999 (first entry)

DE Beta-amyloid peptide derivative A-beta-16-20.

KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;

KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;

KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;

OS Homo sapiens.

OS Synthetic.

PN US5854204-A.

PD 29-DEC-1998.

PF 14-MAR-1996; 96US-0612785.

PR 14-MAR-1996; 96US-0612785.

PR 14-MAR-1995; 95US-0404831.

PR 07-JUN-1995; 95US-0475579.

PR 27-OCT-1995; 95US-0548998.

PA (PRAE-) PRACIS PHARM INC.

PI Benjamin H, Chin J, Pindel's MA, Garnick MB, Gelfer ML;

PI Hundel A, Kasman L, Kelley M, Kubesek W, Lee J;

PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;

DR WPI; 1999-094964/08.

PT New peptide(s) derived from beta-amyloid peptide that inhibit

PT amyloid aggregation - and neurotoxicity, specifically for treatment

PT and prevention of Alzheimer's disease

PS Example 11; Column 63; 52pp; English.

CC The present invention describes beta-amyloid peptide (bap) derivatives.  
 CC The bap derivatives inhibit aggregation of amyloidogenic proteins and  
 CC peptides, specifically bap, and their neurotoxicity, so are useful for  
 CC treating and preventing any disease involving amyloidosis, specifically  
 CC Alzheimer's disease but also Down's syndrome, familial amyloid  
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and  
 CC Creutzfeldt-Jakob disease. The bap derivatives are also used to diagnose  
 CC these diseases, in vitro or in vivo, by detecting binding of bap to  
 CC labelled bap derivatives. Some bap derivatives inhibit bap aggregation  
 CC even when bap is present in molar excess. The present sequence  
 CC represents a bap derivative.

XX Sequence 5 AA;

Query Match 100.0%; Score 4; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Gaps 0;

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QY      1 KLVF 4
Db      1 KLVF 4

RESULT 18
AAAY79937
ID      AAY79937 standard; peptide; 5 AA.
XX      AC      AAY79937;
XX      XX
DT      11-MAY-2000 (first entry)
XX      DE      Beta-amyloid recognition peptide SEQ ID NO:2.
XX      KW      Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;
XX      KW      Alzheimer's disease; neuroprotective; nootropic.
XX      OS      Homo sapiens.
XX      PN      US6022859-A.
XX      PD      08-FEB-2000.
XX      PF      14-NOV-1997; 97US-0970833.
XX      PR      15-NOV-1996; 96US-0030840.
XX      PA      (WISC ) WISCONSIN ALUMNI RES FOUND.
XX      PI      Murphy RM, Kiessling LL;
XX      DR      WPI; 2000-160387/14.
XX      PT      Beta-amyloid inhibitor useful for treating Alzheimer's disease -
XX      PS      Example; Column 7; 15pp; English.
XX      CC      The present invention describes a beta-amyloid inhibitor peptide.
XX      CC      Beta-amyloid inhibitors have neuroprotective and nootropic
XX      CC      properties. The inhibitor peptides are useful for the treatment of
XX      CC      Alzheimer's disease. The present sequence represents a beta-amyloid
XX      CC      recognition peptide used in the exemplification of present invention.
XX      SQ      Sequence 5 AA;
XX      Query Match 100.0%; Score 4; DB 21; Length 5;
XX      Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVF 4
Db      1 KLVF 4

RESULT 19
AAB82629
ID      AAB82629 standard; Peptide; 5 AA.
XX      AC      AAB82629;
XX      XX
DT      02-OCT-2001 (first entry)
XX      DE      All-D peptide used in Alzheimer's disease vaccine.
XX      KW      Alzheimer's disease; amyloidosis; amyloid-related disease;
XX      KW      vaccine; therapy; antigen.
XX      OS      Synthetic.
XX      PH      Key Location/Qualifiers
XX      FT      Misc-difference 1..5

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FT      XX
XX      PN      W0200139796-A2.
XX      PD      07-JUN-2001.
XX      PF      29-NOV-2000; 2000WO-CA01413.
XX      PR      29-NOV-1999; 99US-0168594.
XX      PR      28-NOV-2000; 2000US-0724842.
XX      PA      (NEUR-) NEUROCHEM INC.
XX      PI      Chalifour R, Hebert L, Kong X, Gervais F;
XX      DR      WPI; 2001-441458/47.
XX      PT      Preventing/treating amyloid-related disease, especially Alzheimer's
XX      PT      disease, comprises administering antigenic all-D peptide, e.g. as
XX      PT      vaccine, which elicits production of antibodies to prevent
XX      PT      fibrillogenesis and associated cellular toxicity -
XX      PS      Disclosure; Page 11; 31pp; English.
XX      CC      The present sequence is that of an all-D peptide suitable for
XX      CC      use for preparing vaccines for preventing or treating Alzheimer's
XX      CC      disease and other amyloid related disorders in humans. It is based
XX      CC      on a portion of amyloid-beta peptide (see AAB82622), and may be
XX      CC      modified by removing or inserting 1 or more amino acid residues, or
XX      CC      by substituting 1 or more amino acid residues with other amino acid
XX      CC      residues or non-amino acid fragments. Vaccines of the invention
XX      CC      are produced using 'non-self' peptides synthesised from the
XX      CC      unnatural D-configuration amino acids to avoid the drawbacks of
XX      CC      'self' proteins. The all-D peptides need not be aggregated to be
XX      CC      operative or immunogenic. They preferably interact with at
XX      CC      least 1 region of an amyloid protein, e.g. the beta-sheet region
XX      CC      or GAG-binding site region, the amyloid-beta peptide, or their
XX      CC      immunogenic fragments, protein conjugates, immunogenic derivative
XX      CC      peptides and immunogenic peptidomimetics. Examples include all-D
XX      CC      peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
XX      CC      10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
XX      CC      derivative peptides given in AAB82623-64. The vaccine elicits a
XX      CC      preferential TH-2 or TH-1 response, preventing fibrillogenesis and
XX      CC      associated cellular toxicity. The amyloid related diseases may be
XX      CC      localised amyloidosis, e.g. diabetes type II, neurodegenerative
XX      CC      diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
XX      CC      disease, scrapie, cerebral amyloid angiopathy, and prion protein
XX      CC      related disorders, or systemic amyloidosis associated with chronic
XX      CC      infection (e.g. tuberculosis) or chronic inflammation (e.g.
XX      CC      rheumatoid arthritis), familial Mediterranean fever (FMF) and
XX      CC      systemic amyloidosis found in long-term haemodialysis patients.
XX      SQ      Sequence 5 AA;
XX      Query Match 100.0%; Score 4; DB 22; Length 5;
XX      Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVF 4
Db      1 KLVF 4

RESULT 20
AAB82637
ID      AAB82637 standard; Peptide; 5 AA.
XX      AC      AAB82637;
XX      XX
DT      02-OCT-2001 (first entry)
XX      DE      All-D peptide used in Alzheimer's disease vaccine.
XX      FT

```

KM Alzheimer's disease; amyloidosis; amyloid-related disease;  
 XX vaccine; therapy; antigen.  
 OS Synthetic.  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT Misc-difference 1..5 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 FT  
 XX W0200139796-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 29-NOV-2000; 2000MO-CA01413.  
 XX  
 PR 29-NOV-1999; 99US-0168594.  
 PR 28-NOV-2000; 2000US-0724842.  
 XX  
 XX (NEUR-) NEUROCHEM INC.  
 XX  
 PI Chalfour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 DR  
 XX  
 XX Preventing/creating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, e.g. as  
 PT vaccine, which elicits production of antibodies to prevent  
 PT fibrillogenesis and associated cellular toxicity -  
 XX  
 XX  
 PS Disclosure; Page 11; 31pp; English.  
 XX  
 CC The present sequence is that of an all-D peptide suitable for  
 CC use in preparing vaccines for preventing or treating Alzheimer's  
 CC disease and other amyloid related disorders in humans. It is based  
 CC on a portion of amyloid-beta peptide (see AAB62622), and may be  
 CC modified by removing or inserting 1 or more amino acid residues, or  
 CC by substituting 1 or more amino acid residues with other amino acid  
 CC residues or non-amino acid fragments. Vaccines of the invention  
 CC are produced using 'non-self' peptides synthesised from the  
 CC unnatural D-configuration amino acids to avoid the drawbacks of  
 CC 'self' proteins. The all-D peptides need not be aggregated to be  
 CC operative or immunogenic. They preferably interact with at  
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region  
 CC or GAG-binding site region, the amyloid-beta peptide, or their  
 CC immunogenic fragments, protein conjugates, immunogenic derivative  
 CC peptides and immunogenic peptidomimetics. Examples include all-D  
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,  
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D  
 CC derivative peptides given in AAB62623-64. The vaccine elicits a  
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and  
 CC associated cellular toxicity. The amyloid related diseases may be  
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative  
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob  
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein  
 CC related disorders, or systemic amyloidosis associated with chronic  
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and  
 CC systemic amyloidosis found in long-term haemodialysis patients.  
 XX  
 SQ Sequence 5 AA;  
 XX  
 Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 Db 1 KLVF 4  
 RESULT 21

AAB62803  
 ID AAB62803 standard; peptide; 5 AA.  
 XX  
 XX  
 AC AAB62803;  
 XX  
 XX  
 DT 30-APR-2001 (first entry)  
 DE  
 XX Residues 16-20 of beta-amyloid peptide.  
 XX  
 KM Beta-amyloid peptide; beta-sheet formation inhibitor; neuroprotective;  
 KM antidiabetic; nootropic; anticonvulsant; antiparkinsonian; BSE; kuru;  
 KM ceroidropoietic; Alzheimer's disease; Parkinson's disease;  
 KM bovine spongiform encephalopathy; Creutzfeldt-Jakob disease;  
 KM Huntington's disease; muscular atrophy; spinocerebellar ataxia;  
 KM type II diabetes mellitus; amyloidosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200107474-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000MO-GB02923.  
 XX  
 PR 28-JUL-1999; 99GB-0017725.  
 XX  
 XX (STOR/) STOTT K.  
 PA  
 XX  
 PI Stott K;  
 XX  
 DR WPI; 2001-168537/17.  
 XX  
 XX  
 PT Chemical compound/composition for e.g. treating neurodegenerative  
 PT diseases, comprises peptide comprising Nalpa substituted  
 PT alpha-D-amino-acid residues which inhibit the aggregation of other  
 PT proteins/peptides into beta-sheet -  
 XX  
 XX Example 1; Page 42; 76pp; English.  
 XX  
 CC This invention relates to a peptide containing Nalpa substituted alpha-D  
 CC amino acid residues optionally with Nalpa substituted alpha-D amino  
 CC acids, which is capable of associating specifically with beta-strands  
 CC formed by other protein or peptide molecules and therefore inhibiting  
 CC their aggregation into extended beta-sheets. The peptides exhibit  
 CC neuroprotective; antidiabetic; nootropic; anticonvulsant;  
 CC antiparkinsonian; and cerebroprotective activity. The peptide is used for  
 CC inhibiting or reversing the aggregation of proteins or peptides in vivo  
 CC or in vitro, for assisting in the refolding of denatured or aggregated  
 CC proteins or peptides. The peptides can also be used for in vivo or in  
 CC vitro diagnosis, study or treatment of diseases caused by aggregation of  
 CC proteins or peptides into insoluble beta fibres. The diseases include  
 CC neurodegenerative diseases e.g. Alzheimer's disease, Parkinson's disease,  
 CC prion-related encephalopathies e.g. bovine spongiform encephalopathy  
 CC (BSE) and its human forms Creutzfeldt-Jakob disease and kuru,  
 CC Huntington's disease, X-linked spinal and bulbar muscular atrophy,  
 CC dentatorubral-pallidoluysian atrophy, and at least 5 genetically distinct  
 CC forms of spinocerebellar ataxia; Non-neurodegenerative diseases such as  
 CC type II diabetes mellitus, familial amyloidosis and dialysis-related  
 CC amyloidosis. The present sequence represents a fragment of the  
 CC Alzheimer's disease related beta-amyloid peptide. The peptide is used in  
 CC an example illustrating the use of a peptide of the invention.  
 XX  
 SQ Sequence 5 AA;  
 XX  
 Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 Db 1 KLVF 4

RESULT 22  
 AAB67279  
 ID AAB67279 standard; peptide; 5 AA.  
 XX  
 XX AAB67279;  
 AC  
 XX 20-APR-2001 (first entry)  
 DT  
 XX Residues 16-20 of Alzheimer's Abeta peptide.  
 DE  
 XX Alzheimer's; Abeta; beta-strand.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200107473-A1.  
 PN  
 XX 01-FEB-2001.  
 PD  
 XX 28-JUL-2000; 2000WO-GB02901.  
 PF  
 XX 28-JUL-1999; 99GB-0017724.  
 PR  
 XX (STOT/) STOTT K.  
 PA  
 XX Stott K;  
 PI  
 XX WPI; 2001-182777/18.

Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB 1 KLVP 4  
 Example 1; Page 42; 77pp; English.  
 The present invention relates to a chemical compound or composition comprising a peptide with a beta strand forming section and associated with a target beta-strand formed by a separate peptide-containing molecule. The invention is useful for inhibiting or reversing the association of target beta-strand, formed by Alzheimer's Abeta peptide into a beta-sheet or beta-fibre and the aggregation of proteins or peptides.

Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB 1 KLVP 4

RESULT 23  
 AAB48481  
 ID AAB48481 standard; Peptide; 5 AA.  
 XX  
 XX AAB48481;  
 AC  
 XX 02-MAR-2001 (first entry)  
 DT  
 XX Antifibrillogenic peptide #8.  
 DE  
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200068263-A2.  
 PN  
 XX 16-NOV-2000.

Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB 1 KLVP 4

PF 04-MAY-2000; 2000WO-CA00515.  
 XX  
 PR 05-MAY-1999; 99US-0132592.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 PI Chalifour R, Gervais F, Gupta A;  
 XX  
 DR WPI; 2001-031852/04.  
 XX  
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic -  
 XX  
 PS Claim 7; Page 25; 46pp; English.  
 XX  
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are  
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's  
 CC disease. Peptides AAB48474-B48496 were identified from the  
 CC glycosaminoglycan binding region and the prot-prot interaction region of  
 CC the human amyloid protein.  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB 1 KLVP 4

RESULT 24  
 AAB48489  
 ID AAB48489 standard; Peptide; 5 AA.  
 XX  
 AC AAB48489;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #16.  
 XX  
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 5 /notes= "C-terminal amide"  
 FT  
 XX WO200068263-A2.  
 PN  
 XX 16-NOV-2000.  
 PD  
 XX 04-MAY-2000; 2000WO-CA00515.  
 PF  
 XX 05-MAY-1999; 99US-0132592.  
 PR  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX Chalifour R, Gervais F, Gupta A;  
 PI  
 XX WPI; 2001-031852/04.

Query Match 100.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB 1 KLVP 4

Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 its isomer or peptidomimetic -

PS Claim 7; Page 25; 46pp; English.

XX Peptides ABA8474-B48496 are antifibrinolytic agents that can be used  
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
CC ABA8474-B48496 cause the breakdown of amyloid deposits and are  
CC therefore useful for treating amyloidosis disorders such as Alzheimer's  
CC disease. Peptides ABA8474-B48496 were identified from the  
CC glycosaminoglycan binding region and the prot-prot interaction region of  
CC the human amyloid protein.

XX  
XX

SQL Sequence 5 AA;

Query Match 100.0%; Score 4; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
1 KLVF 4

DB 1 KLVF 4

RESULT 25  
ABA84001  
ID ABA84001 standard; peptide; 5 AA.  
AC ABA84001;  
XX  
XX  
DT 21-AUG-2002 (first entry)  
XX  
DE Transglutaminase inhibitory peptide ap type #1.  
XX  
XX Transglutaminase inhibitor; Factor XIII inhibitor; XIIIa inhibitor;  
XX opthalmological; antiinflammatory; antirheumatic; antiarthritic;  
XX thrombolytic; neuroprotective; nootropic; antiseborrheic; dermatological;  
XX cytostatic; anti-HIV; antiproliferative; cataract; inflammatory disease;  
XX arthritis; thrombosis; Alzheimer's disease; Huntington's chorea;  
XX acne; cancer; HIV infection; psoriasis.

XX  
XX  
OS Unidentified.  
XX  
XX  
PN WO200236798-A2.  
XX  
XX 10-MAY-2002.  
XX  
XX 02-NOV-2001; 2001WO-BP12727.  
XX  
XX 03-NOV-2000; 2000DE-1054687.  
XX  
XX (NZYM-) N ZYME BIOTEC GMBH.  
XX  
XX Fuchsbauer H, Paeternack R, Zotzel U;  
XX  
XX WPI; 2002-444364/47.  
XX  
XX  
XX New amino acid or peptide derivatives or analogs, are selective  
XX transglutaminase inhibitors useful e.g. for treating cataract,  
XX inflammatory diseases, rheumatoid arthritis, thrombosis, Alzheimer's  
XX disease and cancer -  
XX  
XX  
XX Disclosure; Page 13; 44pp; German.

XX  
XX  
XX This invention describes novel amino acid or peptide derivatives or  
XX analogues (I), containing a modified side-chain (e.g. containing a formyl  
XX group) which are transglutaminase inhibitors and Factor XIII/XIIIa  
XX inhibitors. The products of the invention have opthalmological,  
XX antiinflammatory, antirheumatic, antiarthritic, thrombolytic,  
XX neuroprotective, nootropic, antiseborrheic, dermatological, cytoprotective,  
XX anti-HIV and antiproliferative activity. (I) are transglutaminase inhibitors,  
XX especially inhibitors of crosslinking of proteins or peptides  
XX (specifically fibrin and/or alpha-2-plasmin inhibitor) incorporation of  
XX primary amines in proteins and peptides, hydrolysis of the  
XX gamma-carboxamido group of glutamine residues bound in proteins or  
XX peptides, blood factor XIII/XIIIa and mammalian, human, tissue, liver,

CC brain, eye lens, keratinocyte, epidermal, prostate, plant, parasitic  
CC and/or bacterial transglutaminases. The products of the invention can be  
CC used for treating cataract, inflammatory diseases, rheumatoid arthritis,  
CC chronic arthritis, thrombosis, Alzheimer's disease, Huntington's chorea,  
CC acne, cancer (by induction of apoptosis), HIV infections and psoriasis.  
CC (II) Are targeted and specific transglutaminase inhibitors, which can  
CC inhibit a specific type of transglutaminase in the human or animal body  
CC without affecting other transglutaminases. ABA84001-ABA84049 represent  
CC transglutaminase inhibitors described in the method of the invention.

XX  
XX

SQL Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
1 KLVF 4

DB 1 KLVF 4

RESULT 26  
AAU96817  
ID AAU96817 standard; peptide; 5 AA.  
AC AAU96817;  
XX  
XX  
DT 30-JUL-2002 (first entry)  
XX  
XX  
DE Amyloid targeting peptide #7.  
XX  
XX  
XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
XX transmissible cerebral amyloidosis; transmissible virus dementia;  
XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
XX bovine spongiform encephalopathy; inflammation associated amyloid;  
XX primary amyloidosis; feline spongiform encephalopathy;  
XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
XX dialysis-related amyloidosis; light chain-related amyloidosis;  
XX cerebral amyloid angiopathy.

XX  
XX  
OS Synthetic.  
XX  
XX  
XX  
XX Key Location/Qualifiers  
XX  
XX Misc-difference 1..5  
XX  
XX FT  
XX FT  
XX PN WO200207781-A2.  
XX  
XX  
XX 31-JAN-2002.  
XX  
XX  
XX 25-JUL-2001; 2001WO-CA01071.  
XX  
XX  
XX 25-JUL-2000; 2000US-220808P.  
XX  
XX 24-JUL-2001; 2001US-0915092.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX  
XX Gervais F, Kong X, Chalifour R, Migneault D;  
XX  
XX WPI; 2002-371447/40.  
XX  
XX  
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
XX plaques and/or for the treatment of amyloidosis disorders -  
XX  
XX  
XX Claim 49; Page 21; 57pp; English.

XX  
XX  
XX The invention relates to an amyloid-targeting imaging agent comprising  
XX an amyloid targeting moiety, a linker moiety and a labelling moiety.  
XX The agent is of general formula A-t-(A<sub>1</sub>n)<sub>k</sub>-z-A<sub>1</sub>a<sub>1</sub>b<sub>1</sub>(I) where  
XX z = 0-1; A<sub>1</sub>t = an amyloid targeting moiety; A<sub>1</sub>n<sub>k</sub> = a linker  
XX moiety; and A<sub>1</sub>a<sub>1</sub>b<sub>1</sub> = a labelling moiety. Also included are imaging  
XX amyloid deposition or diagnosing an amyloid-related condition in a  
XX patient involving administering (I) to the patient, and ultrasound

CC imaging (I) in the patient to determine the presence of amyloid or  
CC amyloid-related condition; and a kit for preparing a radiopharmaceutical  
CC preparation comprising (I), a reducing agent, a buffering agent, a  
CC transchelating agent, and instructions for the preparation and use of the  
CC radiopharmaceutical in the imaging of amyloid or an amyloid-related  
CC condition. The agents are used for imaging amyloid deposition and for  
CC diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease  
CC (CJD), kuru, transmissible cerebral amyloidosis (transmissible virus  
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
CC non-transmissible cerebral amyloidosis, Alzheimer's disease,  
CC prion-mediated diseases, dialysis-related amyloidosis, light  
CC chain-related amyloidosis, cerebral amyloid angiopathy. The agents are  
CC capable of crossing the blood-brain barrier and are capable of binding  
CC specifically to amyloid plaques. The present sequence is a peptide  
CC forming the amyloid targeting moiety of the agent of the invention.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
|||  
Db 1 KLVP 4

RESULT 27  
AAU96825  
ID AAU96825 standard; peptide; 5 AA.

XX AC AAU96825;

XX DT 30-JUL-2002 (first entry)

XX DE Amyloid targeting peptide #15.

XX KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
KW transmissible cerebral amyloidosis; transmissible virus dementias;  
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
KW bovine spongiform encephalopathy; inflammation associated amyloid;  
KW primary amyloidosis; feline spongiform encephalopathy;  
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
KW dialysis-related amyloidosis; light chain-related amyloidosis;  
KW cerebral amyloid angiopathy.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1..5 /note= "Preferably D-form residue"

FT Modified-site 5 /note= "Phe is amidated"

FT WO200207781-A2.

XX EN 31-JAN-2002.

XX PD 25-JUL-2001; 2001WO-CA01071.

XX PF 25-JUL-2000; 2000US-220808P.

XX PR 24-JUL-2001; 2001US-0915092.

XX XX (NEUR-) NEUROCHEM INC.

XX FA Gervais F, Kong X, Chalifour R, Migneault D;

XX PI WPI; 2002-371447/40.

XX DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid

XX FT plaques and/or for the treatment of amyloidosis disorders -

XX PS Claim 49; Page 21; 57pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent comprising  
CC an amyloid targeting moiety, a linker moiety and a labelling moiety.  
CC The agent is of general formula A\_t-(A\_l\_n\_k)-z-A\_l\_a\_b (I) where  
CC z = 0 - 1; A\_t = an amyloid targeting moiety; A\_l\_n\_k = a linker  
CC moiety; and A\_l\_a\_b = a labelling moiety. Also included are imaging  
CC amyloid deposition or diagnosing an amyloid-related condition in a  
CC patient involving administering (I) to the patient, and ultrasound  
CC imaging (I) in the patient to determine the presence of amyloid or  
CC amyloid-related condition; and a kit for preparing a radiopharmaceutical  
CC preparation comprising (I), a reducing agent, a buffering agent, a  
CC transchelating agent, and instructions for the preparation and use of the  
CC radiopharmaceutical in the imaging of amyloid or an amyloid-related  
CC condition. The agents are used for imaging amyloid deposition and for  
CC diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease  
CC (CJD), kuru, transmissible cerebral amyloidosis (transmissible virus  
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
CC non-transmissible cerebral amyloidosis, Alzheimer's disease,  
CC prion-mediated diseases, dialysis-related amyloidosis, light  
CC chain-related amyloidosis, cerebral amyloid angiopathy. The agents are  
CC capable of crossing the blood-brain barrier and are capable of binding  
CC specifically to amyloid plaques. The present sequence is a peptide  
CC forming the amyloid targeting moiety of the agent of the invention.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
|||  
Db 1 KLVP 4

RESULT 28

AAU11655  
ID AAU11655 standard; Peptide; 5 AA.

XX AC AAU11655;

XX DT 09-APR-2002 (first entry)

XX DE Peptide #8, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX OS Synthetic.

XX PN WO200185093-A2.

XX PD 15-NOV-2001.

XX PF 22-DEC-2000; 2000WO-IB02078.

XX PR 23-DEC-1999; 99US-171877P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Green AM, Gervais F;

XX DR WPI; 2002-075222/10.

XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g.

XX FT Alzheimer's disease comprises contacting blood vessel wall cell with

XX PT amyloid-beta 40 inhibitor -



PS Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral

CC amyloid angiopathy. The new method of the invention involves contacting

CC a blood vessel wall cell with an amyloid-beta40 inhibitor. The invention

CC can be used for treating disease states characterised by cerebral

CC amyloid angiopathy, particularly Alzheimer's disease, hereditary

CC cerebral haemorrhage with amyloidosis of the Dutch type and

CC haemorrhagic stroke. The present sequence represents one of a group

CC of peptides (AAU11648-AAU11669, AAU11910 & AAU11911) that were used in

CC the invention as a carrier for the amyloid-beta40 (Abeta40) inhibitor.

CC The Abeta40 inhibitor was used in the invention to treat a disease

CC state characterised by cerebral amyloid angiopathy (CAA).

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4

Db 1 KLVF 4

RESULT 29

AAU11663

ID AAU11663 standard; Peptide; 5 AA.

XX

AC AAU11663;

XX

DT 09-APR-2002 (first entry)

XX

DE Peptide #16, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX

KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;

KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;

KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Modified-site 5 /note="C-terminal amide"

XX

PN WO200185093-A2.

XX

PD 15-NOV-2001.

XX

XX

PF 22-DEC-2000; 2000WO-IB02078.

XX

XX

PR 23-DEC-1999; 99US-171877P.

XX

XX

PA (NEUR-) NEUROCHEM INC.

XX

PI Green AM, Gervais F;

XX

XX

DR WPI; 2002-075222/10.

XX

PT Inhibiting cerebral amyloid angiopathy used for treating e.g.

PT Alzheimer's disease comprises contacting blood vessel wall cell with

PT amyloid-beta 40 inhibitor -

XX

XX

PS Disclosure; Page 10; 68pp; English.

XX

CC The present invention relates to a new method of inhibiting cerebral

CC amyloid angiopathy. The new method of the invention involves contacting

CC a blood vessel wall cell with an amyloid-beta40 inhibitor. The invention

CC can be used for treating disease states characterised by cerebral

CC amyloid angiopathy, particularly Alzheimer's disease, hereditary

CC cerebral haemorrhage with amyloidosis of the Dutch type and

CC haemorrhagic stroke. The present sequence represents one of a group

CC of peptides (AAU11648-AAU11669, AAU11910 & AAU11911) that were used in

CC the invention as a carrier for the amyloid-beta40 (Abeta40) inhibitor.

CC The Abeta40 inhibitor was used in the invention to treat a disease

CC state characterised by cerebral amyloid angiopathy (CAA).

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4

Db 1 KLVF 4

RESULT 30

ABB05158

ID ABB05158 standard; peptide; 5 AA.

XX

AC ABB05158;

XX

DT 02-APR-2002 (first entry)

XX

DE Beta amyloid peptide (16-20) SEQ ID NO:10.

XX

KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;

KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;

KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;

KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;

KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;

KW amyloidogenic disease; beta amyloid deposition; amyloidosis;

KW hereditary cerebral haemorrhage; familial amyloid polynuropathy.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

PN US6319498-B1.

XX

PD 20-NOV-2001.

XX

XX

PF 14-MAR-1996; 96US-0617267.

XX

XX

PR 14-MAR-1995; 95US-0404831.

PR 07-JUN-1995; 95US-0475579.

PR 27-OCT-1995; 95US-0548998.

XX

XX

PA (PRAE-) PRAECIS PHARM INC.

XX

XX

PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A, Kaeman L;

PI Musso G, Signer ER, Wakefield J, Reed MJ;

XX

DR WPI; 2002-146668/19.

XX

XX

PT Amyloid modulator compound useful for treatment of an amyloidogenic

PT disease such as Alzheimer's disease comprises an aggregation core

PT domain and a modifying group attached to it -

XX

XX

PS Example 11; Column 63; 54pp; English.

XX

CC The present invention describes an amyloid modulator compound (I)

CC comprising an aggregation core domain and a modifying group attached to

CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,

CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic

CC and auditory activities, and can be used as a natural amyloid aggregation

CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide

CC (beta-AP). (I) are used in the manufacture of a medicament for the

CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's

CC disease and other clinical occurrences of beta amyloid deposition such as

CC Down's syndrome individuals and in patients with hereditary cerebral

CC haemorrhage with amyloidosis, and for treating a disorder associated with

CC amyloidosis such as familial amyloid polynuropathy. (I) reduces the

CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)

CC not only reduces the formation of neurotoxic aggregates but also have the

CC ability to reduce the neurotoxicity of performed A-beta fibrils. The  
 CC present sequence represents a beta-AP peptide, which is used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
 ||||  
 Db 1 KLVP 4

RESULT 31  
 ABB05183  
 ID ABB05183 standard; peptide; 5 AA.  
 XX  
 AC ABB05183;  
 XX  
 DT 02-APR-2002 (first entry)  
 XX  
 DE Beta amyloid peptide related peptide PPI-366 SEQ ID NO:37.  
 XX  
 KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;  
 KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;  
 KW neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory;  
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;  
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;  
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;  
 KW hereditary cerebral haemorrhage; familial amyloid polynuropathy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US6319498-B1.  
 XX  
 PD 20-NOV-2001.  
 XX  
 XX 14-MAR-1996; 96US-0617267.  
 PF  
 PR 14-MAR-1995; 95US-0404831.  
 PR 07-JUN-1995; 95US-0475579.  
 PR 27-OCT-1995; 95US-0548998.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 XX  
 PI Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A, Kasman L;  
 PI Musso G, Signer ER, Wakefield J, Reed MJ;  
 XX WPI; 2002-146668/19.  
 DR  
 XX Amyloid modulator compound useful for treatment of an amyloidogenic  
 PT disease such as Alzheimer's disease comprises an aggregation core  
 PT domain and a modifying group attached to it  
 XX  
 XX Example 11; Column 63; 54pp; English.

CC The present invention describes an amyloid modulator compound (I)  
 CC comprising an aggregation core domain and a modifying group attached to  
 CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,  
 CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic  
 CC and auditory activities, and can be used as a natural amyloid aggregation  
 CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide  
 CC (beta-AP). (I) are used in the manufacture of a medicament for the  
 CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's  
 CC disease and other clinical occurrences of beta amyloid deposition such as  
 CC Down's syndrome individuals and in patients with hereditary cerebral  
 CC haemorrhage with amyloidosis, and for treating a disorder associated with  
 CC amyloidosis such as familial amyloid polynuropathy. (I) reduces the  
 CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)  
 CC not only reduces the formation of neurotoxic aggregates but also have the

CC ability to reduce the neurotoxicity of performed A-beta fibrils. The  
 CC present sequence represents a peptide which is used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
 ||||  
 Db 2 KLVP 5

RESULT 32  
 AAW02331  
 ID AAW02331 standard; peptide; 6 AA.  
 XX  
 AC AAW02331;  
 XX  
 DT 02-MAY-1997 (first entry)  
 XX  
 DE Beta-amyloid modulator peptide #22.  
 XX  
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
 KW familial amyloid polynuropathy; familial amyloid cardiomyopathy;  
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deathness;  
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6  
 FT /label= bala  
 XX  
 PN WO9628471-A1.  
 XX  
 PD 19-SEP-1996.  
 XX  
 PF 14-MAR-1996; 96WO-US03492.  
 XX  
 PR 27-OCT-1995; 95US-0548998.  
 PR 14-MAR-1995; 95US-0404831.  
 PR 07-JUN-1995; 95US-0475579.  
 XX  
 PA (PHAR-) PHARM PEPTIDES INC.  
 XX  
 PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;  
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;  
 XX WPI; 1996-433762/43.  
 DR  
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
 PT protein coupled (in)directly to at least 1 modifying gp., useful in  
 PT treatment of Alzheimer's disease  
 XX  
 XX Claim 16; Page 91; 106pp; English.

CC AAW02310-W02332 represent the peptide portions of the beta-amyloid  
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
 CC kilodalton peptide that is the major protein component of amyloid  
 CC plaques. Amyloid plaques are present both in the brain lesions, and in  
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.  
 CC The amyloid modulators of the invention comprise an amyloidogenic protein  
 CC or peptide (such as this sequence) coupled directly or indirectly to at  
 CC least one modifying group. The modifying group is preferably a cyclic,  
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a  
 CC biotin containing group, or a fluorescein containing group. These

CC compound then modulate the aggregation of these sequences to natural  
CC amyloid proteins or peptides when contacted with the natural  
CC amyloidogenic proteins or peptides. The modulator compounds can be used  
CC in the treatment of disorders associated with amyloidosis, such as  
CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,  
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
CC and other types of amyloidosis. The modulators are also useful for the  
CC treatment of disorders associated with beta-amyloidosis, especially  
CC Alzheimer's disease.  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 4; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
Db 1 KLVF 4  
RESULT 33  
AAW02313 standard; peptide; 6 AA.  
XX  
AC AAW02313;  
XX  
DT 02-MAY-1997 (first entry)  
XX  
DE Beta-amyloid modulator peptide #4.  
XX  
KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
KW familial amyloid polynuropathy; familial amyloid cardiomyopathy;  
KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
XX  
OS Synthetic.  
XX  
PN WO9628471-A1.  
XX  
PD 19-SEP-1996.  
XX  
PF 14-MAR-1996; 96WO-US03492.  
XX  
PR 27-OCT-1995; 95US-0548998.  
PR 14-MAR-1995; 95US-0404831.  
PR 07-JUN-1995; 95US-0475579.  
XX  
PA (PHAR-) PHARM PEPTIDES INC.  
XX  
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gelfer ML;  
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;  
XX  
DR WPI; 1996-433762/43.  
XX  
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
PT protein coupled (in)directly to at least 1 modifying gp., useful in  
PT treatment of Alzheimer's disease  
XX  
PS Claim 16; Page 91; 106pp; English.  
XX  
AAW02310-W02332 represent the peptide portions of the beta-amyloid  
CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
CC kilodalton peptide that is the major protein component of amyloid  
CC plaques. Amyloid plaques are present both in the brain lesions, and in  
CC the walls of cerebral blood vessels in Alzheimer's disease patients.

CC The amyloid modulators of the invention comprise an amyloidogenic protein  
CC or peptide (such as this sequence) coupled directly or indirectly to at  
CC least one modifying group. The modifying group is preferably a cyclic,  
CC heterocyclic, or polycyclic group, such as decalin, a cholanlyl group, a  
CC biotin containing group, or a fluorescein containing group. These  
CC compounds then modulate the aggregation of these sequences to natural  
CC amyloid proteins or peptides when contacted with the natural  
CC amyloidogenic proteins or peptides. The modulator compounds can be used  
CC in the treatment of disorders associated with amyloidosis, such as  
CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,  
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
CC and other types of amyloidosis. The modulators are also useful for the  
CC treatment of disorders associated with beta-amyloidosis, especially  
CC Alzheimer's disease.  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 4; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
Db 2 KLVF 5  
RESULT 34  
AAW02314 standard; peptide; 6 AA.  
XX  
AC AAW02314;  
XX  
DT 02-MAY-1997 (first entry)  
XX  
DE Beta-amyloid modulator peptide #5.  
XX  
KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
KW familial amyloid polynuropathy; familial amyloid cardiomyopathy;  
KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
XX  
OS Synthetic.  
XX  
PN WO9628471-A1.  
XX  
PD 19-SEP-1996.  
XX  
PF 14-MAR-1996; 96WO-US03492.  
XX  
PR 27-OCT-1995; 95US-0548998.  
PR 14-MAR-1995; 95US-0404831.  
PR 07-JUN-1995; 95US-0475579.  
XX  
PA (PHAR-) PHARM PEPTIDES INC.  
XX  
PI Benjamin H, Chin J, Findeis MA, Garnick MB, Gelfer ML;  
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;  
XX  
DR WPI; 1996-433762/43.  
XX  
PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
PT protein coupled (in)directly to at least 1 modifying gp., useful in  
PT treatment of Alzheimer's disease  
XX  
PS Claim 16; Page 91; 106pp; English.  
XX

CC AAW02310-W02332 represent the peptide portions of the beta-amyloid  
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
 CC kilodalton peptide that is the major protein component of amyloid  
 CC plaques. Amyloid plaques are present both in the brain lesions, and in  
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.  
 CC The amyloid modulators of the invention comprise an amyloidogenic protein  
 CC or peptide (such as this sequence) coupled directly or indirectly to at  
 CC least one modifying group. The modifying group is preferably a cyclic,  
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a  
 CC biotin containing group, or a fluorescein containing group. These  
 CC compounds then modulate the aggregation of these sequences to natural  
 CC amyloid proteins or peptides when contacted with the natural  
 CC amyloidogenic proteins or peptides. The modulator compounds can be used  
 CC in the treatment of disorders associated with amyloidosis, such as  
 CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,  
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
 CC and other types of amyloidosis. The modulators are also useful for the  
 CC treatment of disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease.

XX Sequence 6 AA;  
 SQ

Query Match 100.0%; Score 4; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 1 KLVF 4

#### RESULT 35

AAW45944  
 ID AAW45944 standard; peptide; 6 AA.

XX AAW45944;

XX 30-JUN-1998 (first entry)

XX Amyloid beta peptide fragment.

XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
 XX positron emission tomography; PET; Down's syndrome; amyloidosis.

XX Homo sapiens.

XX WO9721728-A1.

XX 19-JUN-1997.

XX 09-DEC-1996; 96WO-SE01621.

XX 29-DEC-1995; 95US-0009386.

XX 12-DEC-1995; 95SE-0004467.

XX (KARO-) KAROLINSKA INNOVATIONS AB.

XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

XX WPI; 1997-332723/30.

XX Use of new and known peptide(s) for inhibition of polymerisation of  
 XX amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
 XX Down's syndrome associated with amyloidosis.

XX Example 1; Figure 2B; 31pp; English.

XX This sequence represents a fragment of the amyloid beta peptide. The  
 XX invention relates to the use of peptide compounds for inhibition of  
 XX polymerisation of amyloid beta peptide (ABP), as model substances for

CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a  
 CC tool for the identification of other organic compounds with similar  
 CC functional properties, or as ligands in positron emission tomography.  
 CC The peptides may be used in treatment of amyloidosis, especially in  
 CC treatment of Alzheimer's disease associated with amyloidosis, for  
 CC treatment or prevention of demens in patients with Down's syndrome, for  
 CC treatment or prevention of hereditary cerebral haemorrhage with  
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of  
 CC human amyloid protein. They can also be used for identifying other  
 CC molecules with similar properties and/or as ligands for detection of  
 CC amyloid deposits using e.g. positron emission tomography.

XX Sequence 6 AA;

Query Match 100.0%; Score 4; DB 18; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 2 KLVF 5

#### RESULT 36

AAW45945  
 ID AAW45945 standard; peptide; 6 AA.

XX AAW45945;

XX 30-JUN-1998 (first entry)

XX Amyloid beta peptide fragment.

XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
 XX positron emission tomography; PET; Down's syndrome; amyloidosis.

XX Homo sapiens.

XX WO9721728-A1.

XX 19-JUN-1997.

XX 09-DEC-1996; 96WO-SE01621.

XX 29-DEC-1995; 95US-0009386.

XX 12-DEC-1995; 95SE-0004467.

XX (KARO-) KAROLINSKA INNOVATIONS AB.

XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

XX WPI; 1997-332723/30.

XX Use of new and known peptide(s) for inhibition of polymerisation of  
 XX amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
 XX Down's syndrome associated with amyloidosis.

XX Example 1; Figure 2B; 31pp; English.

XX This sequence represents a fragment of the amyloid beta peptide. The  
 XX invention relates to the use of peptide compounds for inhibition of  
 XX polymerisation of amyloid beta peptide (ABP), as model substances for  
 XX synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a  
 XX tool for the identification of other organic compounds with similar  
 XX functional properties, or as ligands in positron emission tomography.  
 XX The peptides may be used in treatment of amyloidosis, especially in  
 XX treatment of Alzheimer's disease associated with amyloidosis, for  
 XX treatment or prevention of demens in patients with Down's syndrome, for  
 XX treatment or prevention of hereditary cerebral haemorrhage with  
 XX amyloidosis (Dutch type) or for the prevention of fibril formation of  
 XX human amyloid protein. They can also be used for identifying other  
 XX molecules with similar properties and/or as ligands for detection of  
 XX amyloid deposits using e.g. positron emission tomography.

```

XX Sequence 6 AA;
SQ Query Match 100.0%; Score 4; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 3 KLVF 6

RESULT 37
AAW29090
ID AAW29090 standard; peptide; 6 AA.
XX
XX AAW29090;
AC
XX
XX 20-UTL-1999 (first entry)
DT
XX
XX A-beta-binding peptide fragment conjugated to cyclosporin.
DE
XX
XX Cyclosporin; A-beta peptide; conjugate; neurological disease;
KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;
KW ALS; non-immunosuppressive; amyloid plaque formation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 6
FT /note= "The C-terminal is condensed onto the side
FT chain of Lys (7) of the cyclosporin analog described
FT in AAW29087, AAW29088, AAW29095 and AAW29097"
XX
XX MO910374-A1.
PN
XX
XX 04-MAR-1999.
PD
XX
XX 25-AUG-1998; 98WO-US17544.
PF
XX
XX 26-AUG-1997; 97US-0057751.
PR
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
PA
XX
XX Rich DH, Solomon ME;
PI
XX
XX WPI; 1999-276928/23.
DR
XX
XX New A-beta-binding peptide conjugates and CSA analogs - useful in
PT treatment of neurological diseases e.g. Alzheimer's disease,
PT multiple sclerosis etc.
XX
XX Claim 5; Page 98; 129pp; English.
PS
XX
XX New conjugates are disclosed which are of formula A-Z, in which: A is
CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506
CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more
CC contiguous residues of A-beta peptide. The compounds are novel chemical
CC inducers of dimerization which are non-immunosuppressive and which are
CC inhibitors of A-beta peptide aggregation and deposition in amyloid
CC plaques. The adverse consequences of amyloid plaque formation can be
CC prevented or ameliorated by sequestering the A-beta peptide in monomeric
CC form with a conjugate which links the A-beta to cyclophilin or FKBP,
CC therefore providing a mechanism to minimize the amount of free A-beta
CC available for fibril formation and deposition. The compounds can be used
CC for the treatment of Alzheimer's disease, multiple sclerosis and
CC amyotrophic lateral sclerosis.
XX
XX Sequence 6 AA;
SQ Query Match 100.0%; Score 4; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KLVF 4
Db 2 KLVF 5

RESULT 38
AAW29091
ID AAW29091 standard; peptide; 6 AA.
XX
XX AAW29091;
AC
XX
XX 20-UTL-1999 (first entry)
DT
XX
XX A-beta-binding peptide fragment conjugated to cyclosporin.
DE
XX
XX Cyclosporin; A-beta peptide; conjugate; neurological disease;
KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;
KW ALS; non-immunosuppressive; amyloid plaque formation.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 6
FT /note= "The C-terminal is condensed onto the side
FT chain of Lys (7) of the cyclosporin analog described
FT in AAW29087, AAW29088, AAW29095 and AAW29097"
XX
XX MO910374-A1.
PN
XX
XX 04-MAR-1999.
PD
XX
XX 25-AUG-1998; 98WO-US17544.
PF
XX
XX 26-AUG-1997; 97US-0057751.
PR
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
PA
XX
XX Rich DH, Solomon ME;
PI
XX
XX WPI; 1999-276928/23.
DR
XX
XX New A-beta-binding peptide conjugates and CSA analogs - useful in
PT treatment of neurological diseases e.g. Alzheimer's disease,
PT multiple sclerosis etc.
XX
XX Claim 5; Page 98; 129pp; English.
PS
XX
XX New conjugates are disclosed which are of formula A-Z, in which: A is
CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506
CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more
CC contiguous residues of A-beta peptide. The compounds are novel chemical
CC inducers of dimerization which are non-immunosuppressive and which are
CC inhibitors of A-beta peptide aggregation and deposition in amyloid
CC plaques. The adverse consequences of amyloid plaque formation can be
CC prevented or ameliorated by sequestering the A-beta peptide in monomeric
CC form with a conjugate which links the A-beta to cyclophilin or FKBP,
CC therefore providing a mechanism to minimize the amount of free A-beta
CC available for fibril formation and deposition. The compounds can be used
CC for the treatment of Alzheimer's disease, multiple sclerosis and
CC amyotrophic lateral sclerosis.
XX
XX Sequence 6 AA;
SQ Query Match 100.0%; Score 4; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 39  
AAW29092  
ID AAW29092 standard; peptide; 6 AA.  
XX  
AC AAW29092;  
XX  
XX 20-JUL-1999 (first entry)  
DT  
XX  
XX A-beta-binding peptide fragment conjugated to cyclosporin.  
DE  
XX  
XX Cyclosporin; A-beta peptide; conjugate; neurological disease;  
KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;  
KW AUS; non-immunosuppressive; amyloid plaque formation.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
PH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "The omega-COOH group of Glu(1) is condensed  
FT onto the side chain of Lys(7) of the cyclosporin analog  
FT described in AAW29087, AAW29088, AAW29095 and AAW29097"  
XX  
XX WO9910374-A1.  
XX  
XX 04-MAR-1999.  
XX  
XX 25-AUG-1998; 98WO-US17544.  
XX  
XX 26-AUG-1997; 97US-0057751.  
XX  
XX (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX  
XX Rich DH, Solomon ME;  
XX  
XX WPI; 1999-276928/23.  
XX  
XX New A-beta-binding peptide conjugates and Csa analogs - useful in  
FT treatment of neurological diseases e.g. Alzheimer's disease,  
FT multiple sclerosis etc.  
XX  
XX Claim 5; Page 98; 129pp; English.  
XX  
XX New conjugates are disclosed which are of formula A-Z, in which: A is  
CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506  
CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more  
CC contiguous residues of A-beta peptide. The compounds are novel chemical  
CC inducers of dimerization which are non-immunosuppressive and which are  
CC inhibitors of A-beta peptide aggregation and deposition in amyloid  
CC plaques. The adverse consequences of amyloid plaque formation can be  
CC prevented or ameliorated by sequestering the A-beta peptide in monomeric  
CC form with a conjugate which links the A-beta to cyclophilin or FKBP,  
CC therefore providing a mechanism to minimize the amount of free A-beta  
CC available for fibril formation and deposition. The compounds can be used  
CC for the treatment of Alzheimer's disease, multiple sclerosis and  
CC amyotrophic lateral sclerosis.  
XX  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 4; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KLVP 4  
Db 2 KLVP 5  
RESULT 40  
AAW89388  
ID AAW89388 standard; peptide; 6 AA.  
XX  
XX  
AC AAW89388;  
XX

02-MAR-1999 (first entry)  
DT  
XX  
XX Beta-amyloid peptide derivative A-beta-16-21 (A21 to beta-A).  
DE  
XX  
XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;  
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;  
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;  
KW Creutzfeldt-Jakob disease; BAP.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 6  
FT /note= "beta-alanyl"  
XX  
XX US5854204-A.  
XX  
XX 29-DEC-1998.  
XX  
XX 14-MAR-1996; 96US-0612785.  
XX  
XX 14-MAR-1996; 96US-0612785.  
XX  
XX 14-MAR-1995; 95US-0404831.  
XX  
XX 07-JUN-1995; 95US-0475579.  
XX  
XX 27-OCT-1995; 95US-0548998.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
XX  
XX Benjamin H, Chin J, Findeis MA, Garnick MB, Gefter ML;  
XX Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
XX Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;  
XX WPI; 1999-094964/08.  
XX  
XX New peptide(s) derived from beta-amyloid peptide that inhibit  
PT amyloid aggregation - and neurotoxicity, specifically for treatment  
PT and prevention of Alzheimer's disease  
XX  
XX Example 12; Column 64; 52pp; English.  
XX  
XX The present invention describes beta-amyloid peptide (BAP) derivatives.  
XX The BAP derivatives inhibit aggregation of amyloidogenic proteins and  
XX peptides, specifically BAP, and their neurotoxicity, so are useful for  
XX treating and preventing any disease involving amyloidosis, specifically  
XX Alzheimer's disease but also Down's syndrome, familial amyloid  
XX polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and  
XX Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose  
XX these diseases, in vitro or in vivo, by detecting binding of BAP to  
XX labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation  
XX even when BAP is present in molar excess. The present sequence  
XX represents a BAP derivative.  
XX  
XX Sequence 6 AA;  
Query Match 100.0%; Score 4; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KLVP 4  
Db 1 KLVP 4  
Search completed: January 3, 2003, 07:52:00  
Job time : 57 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:44:41 ; Search time 164 Seconds  
(without alignments)  
0.462 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 19

Sequence: 1 KLVF 4

Scoring table: BLOSUM62  
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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	10	US-09-867-847-15
2	19	100.0	4	10	US-09-867-847-23
3	19	100.0	4	10	US-09-850-061A-25
4	19	100.0	5	10	US-09-867-847-17
5	19	100.0	5	10	US-09-867-847-25
6	19	100.0	5	10	US-09-850-061A-19
7	19	100.0	5	10	US-09-850-061A-19
8	19	100.0	5	10	US-09-850-061A-43
9	19	100.0	5	10	US-09-972-475-10
10	19	100.0	5	10	US-09-972-475-37
11	19	100.0	6	10	US-09-867-847-7
12	19	100.0	6	10	US-09-867-847-20
13	19	100.0	6	10	US-09-867-847-52
14	19	100.0	6	10	US-09-867-847-55
15	19	100.0	6	10	US-09-867-847-58
16	19	100.0	6	10	US-09-867-847-61
17	19	100.0	6	10	US-09-867-847-64
18	19	100.0	6	10	US-09-850-061A-5
19	19	100.0	6	10	US-09-850-061A-15

20	19	100.0	6	10	US-09-972-475-8	Sequence 8, Appli
21	19	100.0	6	10	US-09-972-475-9	Sequence 9, Appli
22	19	100.0	6	10	US-09-972-475-31	Sequence 31, Appli
23	19	100.0	6	10	US-09-972-475-43	Sequence 43, Appli
24	19	100.0	6	10	US-09-956-625-25	Sequence 25, Appli
25	19	100.0	7	10	US-09-867-847-12	Sequence 12, Appli
26	19	100.0	7	10	US-09-867-847-27	Sequence 27, Appli
27	19	100.0	7	10	US-09-867-847-28	Sequence 28, Appli
28	19	100.0	7	10	US-09-850-061A-11	Sequence 11, Appli
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32	19	100.0	8	10	US-09-850-061A-9	Sequence 9, Appli
33	19	100.0	8	10	US-09-850-061A-14	Sequence 14, Appli
34	19	100.0	8	10	US-09-972-475-5	Sequence 5, Appli
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36	19	100.0	9	10	US-09-867-847-9	Sequence 9, Appli
37	19	100.0	9	10	US-09-850-061A-6	Sequence 6, Appli
38	19	100.0	9	10	US-09-850-061A-7	Sequence 7, Appli
39	19	100.0	10	10	US-09-867-847-29	Sequence 29, Appli
40	19	100.0	10	10	US-09-850-061A-2	Sequence 2, Appli
41	19	100.0	11	10	US-09-988-842-9	Sequence 9, Appli
42	19	100.0	11	10	US-09-988-842-25	Sequence 25, Appli
43	19	100.0	12	10	US-09-867-847-8	Sequence 8, Appli
44	19	100.0	12	10	US-09-922-800-5	Sequence 5, Appli
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#### ALIGNMENTS

RESULT 1  
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; Sequence 15, Application US/09867847  
; Patent No. US20020094335A1  
GENERAL INFORMATION:  
; APPLICANT: Chailifour, Robert  
; APPLICANT: Hebert, Lisa  
; APPLICANT: Kong, Xiang  
; APPLICANT: Gervais, Francine  
TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
FILE REFERENCE: 1445-501 CIP  
CURRENT FILING DATE: 2001-09-20  
PRIOR APPLICATION NUMBER: US/09/867,847  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: 09/724,842  
PRIOR FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
OTHER INFORMATION: or peptidomimetics  
US-09-867-847-15  
Query Match 100.0%; Score 19; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
DB 1 KLVF 4  
RESULT 2  
US-09-867-847-23  
; Sequence 23, Application US/09867847  
; Patent No. US20020094335A1

```

; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: AMIDATION
; US-09-867-847-23

Query Match 100.0%; Score 19; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 1 KLVF 4

RESULT 3
US-09-850-061A-25
; Sequence 25, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERNETUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850,061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Amyloidosis
; US-09-850-061A-25

Query Match 100.0%; Score 19; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 1 KLVF 4

; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: AMIDATION
; US-09-867-847-23

Query Match 100.0%; Score 19; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 1 KLVF 4

RESULT 4
US-09-867-847-17
; Sequence 17, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; US-09-867-847-17

Query Match 100.0%; Score 19; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 1 KLVF 4

RESULT 5
US-09-867-847-25
; Sequence 25, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: AMIDATION
; US-09-867-847-25
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Query Match 100.0%; Score 19; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 Db 1 KLVF 4

RESULT 6  
 US-09-850-061A-1  
 ; Sequence 1, Application US/09850061A  
 ; Patent No. US20020094957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NORDSTEDT, Christer  
 ; APPLICANT: NASLUND, Jan  
 ; APPLICANT: THYBERG, Johan  
 ; APPLICANT: TJERNBERG, Lars O.  
 ; APPLICANT: TERNIUS, Lars  
 ; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
 ; FILE REFERENCE: 03315-002  
 ; CURRENT APPLICATION NUMBER: US/09/850,061A  
 ; CURRENT FILING DATE: 2001-05-08  
 ; PRIOR APPLICATION NUMBER: US 09/095,106  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
 ; PRIOR FILING DATE: 1996-12-09  
 ; PRIOR APPLICATION NUMBER: SE 9504467-3  
 ; PRIOR FILING DATE: 1995-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/009,386  
 ; PRIOR FILING DATE: 1995-12-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Amyloidosis  
 ; US-09-850-061A-1

Query Match 100.0%; Score 19; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 Db 1 KLVF 4

RESULT 7  
 US-09-850-061A-19  
 ; Sequence 19, Application US/09850061A  
 ; Patent No. US20020094957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NORDSTEDT, Christer  
 ; APPLICANT: NASLUND, Jan  
 ; APPLICANT: THYBERG, Johan  
 ; APPLICANT: TJERNBERG, Lars O.  
 ; APPLICANT: TERNIUS, Lars  
 ; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
 ; FILE REFERENCE: 03315-002  
 ; CURRENT APPLICATION NUMBER: US/09/850,061A  
 ; CURRENT FILING DATE: 2001-05-08  
 ; PRIOR APPLICATION NUMBER: US 09/095,106  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
 ; PRIOR FILING DATE: 1996-12-09  
 ; PRIOR APPLICATION NUMBER: SE 9504467-3  
 ; PRIOR FILING DATE: 1995-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/009,386  
 ; PRIOR FILING DATE: 1995-12-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 19

LENGTH: 5  
 TYPE: PRT  
 ORGANISM: Amyloidosis  
 US-09-850-061A-19

Query Match 100.0%; Score 19; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 Db 2 KLVF 5

RESULT 8  
 US-09-850-061A-43  
 ; Sequence 43, Application US/09850061A  
 ; Patent No. US20020094957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NORDSTEDT, Christer  
 ; APPLICANT: NASLUND, Jan  
 ; APPLICANT: THYBERG, Johan  
 ; APPLICANT: TJERNBERG, Lars O.  
 ; APPLICANT: TERNIUS, Lars  
 ; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
 ; FILE REFERENCE: 03315-002  
 ; CURRENT APPLICATION NUMBER: US/09/850,061A  
 ; CURRENT FILING DATE: 2001-05-08  
 ; PRIOR APPLICATION NUMBER: US 09/095,106  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
 ; PRIOR FILING DATE: 1996-12-09  
 ; PRIOR APPLICATION NUMBER: SE 9504467-3  
 ; PRIOR FILING DATE: 1995-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/009,386  
 ; PRIOR FILING DATE: 1995-12-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 43  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Amyloidosis  
 ; US-09-850-061A-43

Query Match 100.0%; Score 19; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 Db 1 KLVF 4

RESULT 9  
 US-09-972-475-10  
 ; Sequence 10, Application US/09972475  
 ; Patent No. US20020098173A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Findeis, Mark A. et al.  
 ; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
 ; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25



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; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)_
; OTHER INFORMATION: AMIDATION
US-09-867-847-20

Query Match          100.0%; Score 19; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 13
US-09-867-847-52
; Sequence 52, Application US/09867847
; Patent No. US2002009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 52
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-52

Query Match          100.0%; Score 19; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 14
US-09-867-847-55
; Sequence 55, Application US/09867847
; Patent No. US2002009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
```

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; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 55
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-55

Query Match          100.0%; Score 19; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 15
US-09-867-847-58
; Sequence 58, Application US/09867847
; Patent No. US2002009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 58
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (4)-(5)
; OTHER INFORMATION: Xaa is thienylalanine
US-09-867-847-58

Query Match          100.0%; Score 19; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

Search completed: January 3, 2003, 07:50:57
Job time : 165 secs
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CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US98 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US98 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US98 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-617-267C-37

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 2 KLVF 5

RESULT 12  
US-09-095-106A-1  
Sequence 1, Application US/09095106A  
Patent No. 6331440  
GENERAL INFORMATION:  
APPLICANT: NORDSTEDT, Christer  
APPLICANT: NASLUND, Jan  
APPLICANT: THYBERG, Johan  
APPLICANT: TERNBERG, Lars O.  
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
FILE REFERENCE: 000500-124  
CURRENT APPLICATION NUMBER: US/09/095,106A  
FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: US 60/009,386  
PRIOR FILING DATE: 1995-12-29  
PRIOR APPLICATION NUMBER: PCT/SE96/01621  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Amyloidosis  
US-09-095-106A-1

Query Match 100.0%; Score 19; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
|||  
Db 2 KLVF 4

RESULT 13  
US-09-095-106A-19  
Sequence 19, Application US/09095106A  
Patent No. 6331440  
GENERAL INFORMATION:  
APPLICANT: NORDSTEDT, Christer  
APPLICANT: NASLUND, Jan  
APPLICANT: THYBERG, Johan  
APPLICANT: TERNBERG, Lars O.  
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
FILE REFERENCE: 000500-124  
CURRENT APPLICATION NUMBER: US/09/095,106A  
FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: US 60/009,386  
PRIOR FILING DATE: 1995-12-29  
PRIOR APPLICATION NUMBER: PCT/SE96/01621  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 19  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Amyloidosis  
US-09-095-106A-19

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 2 KLVF 5

RESULT 14  
US-09-095-106A-43  
Sequence 43, Application US/09095106A  
Patent No. 6331440  
GENERAL INFORMATION:  
APPLICANT: NORDSTEDT, Christer  
APPLICANT: NASLUND, Jan  
APPLICANT: THYBERG, Johan  
APPLICANT: TERNBERG, Lars O.  
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
FILE REFERENCE: 000500-124  
CURRENT APPLICATION NUMBER: US/09/095,106A  
FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: US 60/009,386  
PRIOR FILING DATE: 1995-12-29  
PRIOR APPLICATION NUMBER: PCT/SE96/01621  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 43  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Amyloidosis  
US-09-095-106A-43

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVF 4  
|  
|  
|  
|  
Db 1 KLVF 4

## RESULT 15

PCT-US94-10475-15  
; Sequence 15, Application PC/TUS9410475  
; GENERAL INFORMATION:  
; APPLICANT: Eugene Roberts  
; TITLE OF INVENTION: Method For  
; TITLE OF INVENTION: Antagonizing Amnestic  
; TITLE OF INVENTION: Effects of Amyloid n  
; TITLE OF INVENTION: Protein and Improving  
; TITLE OF INVENTION: the Quality of Life  
; TITLE OF INVENTION: in Individuals  
; TITLE OF INVENTION: With Alzheimer Disease  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: City of Hope  
; STREET: 1500 East Duarte Road  
; CITY: Duarte  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91010-0269  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3M Double Density 5 1/4"  
; MEDIUM TYPE: diskette  
; COMPUTER: Wang PC  
; OPERATING SYSTEM: MS DOS Version 3.20  
; SOFTWARE: Microsoft  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/10475  
; FILING DATE: 16 September 1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: U. S. Application  
; PRIOR APPLICATION DATA: Serial No.  
; PRIOR APPLICATION DATA: 08/127,904; filed  
; PRIOR APPLICATION DATA: 29 September 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Irons, Edward S.  
; REGISTRATION NUMBER: 16,541  
; REFERENCE/DOCKET NUMBER: None  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 626-3564 or 783-6030  
; TELEFAX: (202) 783-6031  
; TELEX: None  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: Amino Acid  
; STRANDEDNESS:  
; TOPOLOGY: Unknown  
; PCT-US94-10475-15

Query Match 100.0%; Score 19; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVF 4  
|  
|  
|  
|  
Db 1 KLVF 4

Search completed: January 3, 2003, 07:45:19  
Job time : 16 secs

TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Decontii, Giulio A.  
REGISTRATION NUMBER: 31,583  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-10

Query Match 100.0%; Score 19; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 6  
US-08-970-833-2  
Sequence 2, Application US/08970833  
Patent No. 6022859  
GENERAL INFORMATION:  
APPLICANT: Kieselring, Laura L.  
APPLICANT: Murphy, Regina M.  
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles & Brady  
STREET: 411 East Wisconsin Avenue  
CITY: Milwaukee  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53202-4497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,833  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Baker, Jean C.  
REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 960296.94291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (414) 277-5709  
TELEFAX: (414) 271-3552  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-970-833-2

Query Match 100.0%; Score 19; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 7  
US-08-703-675C-46  
Sequence 46, Application US/08703675C  
Patent No. 6303567  
GENERAL INFORMATION:  
APPLICANT: Fideis, Mark A. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703,675C  
FILING DATE: 27-AUG-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: PPI-016CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 46:

Aggregation Comprising D-

;; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-703-675C-46

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 1 KLVF 4

RESULT 8  
US-09-242-724-25  
; Sequence 25, Application US/09242724  
; Patent No. 6316405  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, Michael E.  
; APPLICANT: Rich, Daniel H.  
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor  
; FILE REFERENCE: Cyclosporin Analogs  
; CURRENT APPLICATION NUMBER: US/09/242,724  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn-Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ;  
US-09-242-724-25

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 9  
US-09-242-724-26  
; Sequence 26, Application US/09242724  
; Patent No. 6316405  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, Michael E.  
; APPLICANT: Rich, Daniel H.  
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor  
; FILE REFERENCE: Cyclosporin Analogs  
; CURRENT APPLICATION NUMBER: US/09/242,724  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)-  
; OTHER INFORMATION: ACETYLATION; K(2Cl-Cbz) =  
; OTHER INFORMATION: 2-chlorobenzoyloxycarbonyl-protected lysine  
US-09-242-724-26

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 1 KLVF 4

RESULT 10  
US-08-617-267C-10  
; Sequence 10, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findels, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-617-267C-10

Query Match 100.0%; Score 19; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 11  
US-08-617-267C-37  
; Sequence 37, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findels, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street



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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:43:01 ; Search time 15 Seconds  
(without alignments)  
7.846 Million cell updates/sec

Title: US-09-867-847-15

Sequence: 1 KLVF 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	US-08-970-833-1	Sequence 1, Appl
2	19	100.0	4	US-08-664-379B-17	Sequence 17, Appl
3	19	100.0	4	US-09-095-106A-25	Sequence 25, Appl
4	19	100.0	5	US-08-127-904-15	Sequence 15, Appl
5	19	100.0	5	US-08-612-785B-10	Sequence 10, Appl
6	19	100.0	5	US-08-970-833-2	Sequence 2, Appl
7	19	100.0	5	US-08-703-675C-46	Sequence 46, Appl
8	19	100.0	5	US-09-242-724-25	Sequence 25, Appl
9	19	100.0	5	US-09-242-724-26	Sequence 26, Appl
10	19	100.0	5	US-08-617-267C-10	Sequence 10, Appl
11	19	100.0	5	US-08-617-267C-37	Sequence 37, Appl
12	19	100.0	5	US-09-095-106A-1	Sequence 1, Appl
13	19	100.0	5	US-09-095-106A-19	Sequence 19, Appl
14	19	100.0	5	US-09-095-106A-43	Sequence 43, Appl
15	19	100.0	5	PCT-US94-10475-15	Sequence 15, Appl
16	19	100.0	6	US-08-612-785B-8	Sequence 8, Appl
17	19	100.0	6	US-08-612-785B-9	Sequence 9, Appl
18	19	100.0	6	US-08-612-785B-31	Sequence 31, Appl
19	19	100.0	6	US-08-664-379B-19	Sequence 19, Appl
20	19	100.0	6	US-08-703-675C-31	Sequence 31, Appl
21	19	100.0	6	US-08-703-675C-32	Sequence 32, Appl
22	19	100.0	6	US-08-703-675C-44	Sequence 44, Appl
23	19	100.0	6	US-09-242-724-27	Sequence 27, Appl
24	19	100.0	6	US-09-242-724-30	Sequence 30, Appl
25	19	100.0	6	US-09-242-724-31	Sequence 31, Appl
26	19	100.0	6	US-09-242-724-31	Sequence 31, Appl
27	19	100.0	6	US-09-242-724-33	Sequence 33, Appl

28	19	100.0	6	US-08-617-267C-8	Sequence 8, Appl
29	19	100.0	6	US-08-617-267C-9	Sequence 9, Appl
30	19	100.0	6	US-08-617-267C-31	Sequence 31, Appl
31	19	100.0	6	US-08-617-267C-43	Sequence 43, Appl
32	19	100.0	6	US-09-095-106A-5	Sequence 5, Appl
33	19	100.0	6	US-09-095-106A-15	Sequence 15, Appl
34	19	100.0	7	US-08-127-904-14	Sequence 14, Appl
35	19	100.0	7	US-08-612-785B-6	Sequence 6, Appl
36	19	100.0	7	US-08-612-785B-7	Sequence 7, Appl
37	19	100.0	7	US-08-703-675C-29	Sequence 29, Appl
38	19	100.0	7	US-08-703-675C-30	Sequence 30, Appl
39	19	100.0	7	US-08-617-267C-6	Sequence 6, Appl
40	19	100.0	7	US-08-617-267C-7	Sequence 7, Appl
41	19	100.0	7	US-09-264-709A-13	Sequence 13, Appl
42	19	100.0	7	US-09-095-106A-11	Sequence 11, Appl
43	19	100.0	7	US-09-095-106A-12	Sequence 12, Appl
44	19	100.0	7	PCT-US94-10475-14	Sequence 14, Appl
45	19	100.0	8	US-08-457-804-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-970-833-1  
; Sequence 1, Application: US/08970833  
; Patent No. 6022859  
; GENERAL INFORMATION:  
; APPLICANT: Klesling, Laura L.  
; APPLICANT: Murphy, Regina M.  
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/970, 833  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 960296.94291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5709  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-970-833-1

Query Match 100.0%; Score 19; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
DB 1 KLVF 4

RESULT 2  
US-08-664-379B-17  
; Sequence 17, Application US/08664379B  
; Patent No. 6034211  
; GENERAL INFORMATION:  
; APPLICANT: Kelly, Jeffery W.  
; TITLE OF INVENTION: BETA-SHEET NUCLEATING PEPTIDOMIMETICS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/664,379B  
; FILING DATE: 14-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/018,925  
; FILING DATE: 03-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 08435/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-664-379B-17

Query Match 100.0%; Score 19; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 3  
US-09-095-106A-25  
; Sequence 25, Application US/09095106A  
; Patent No. 6331440  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: THYBERG, Johan  
; APPLICANT: TUERNBERG, Lars O.  
; APPLICANT: TERENIUS, Lars  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 000500-124  
; CURRENT APPLICATION NUMBER: US/09/095,106A  
; CURRENT FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29  
; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
; PRIOR FILING DATE: 1996-12-09  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 4

; TYPE: PRT  
; ORGANISM: Amyloidosis  
US-09-095-106A-25

Query Match 100.0%; Score 19; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 4  
US-08-127-904-15  
; Sequence 15, Application US/08127904  
; Patent No. 5470951  
; GENERAL INFORMATION:  
; APPLICANT: Eugene Roberts  
; TITLE OF INVENTION: Method For Antagonizing  
; TITLE OF INVENTION: Amnestic Effects of Amyloid n  
; TITLE OF INVENTION: Protein and Improving the  
; TITLE OF INVENTION: Quality of Life in Individuals  
; TITLE OF INVENTION: With Alzheimer Disease  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: City of Hope  
; STREET: 1500 East Duarte Road  
; CITY: Duarte  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91010-0269  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3M-Double Density 5 1/4" diskette  
; COMPUTER: Wang PC  
; OPERATING SYSTEM: MS DOS Version 3.20  
; SOFTWARE: Microsoft  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,904  
; FILING DATE: 29 September 1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA: No. 5470951e  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Itons, Edward S.  
; REGISTRATION NUMBER: 16,541  
; REFERENCE/DOCKET NUMBER: No. 5470951e  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; TELEX: No. 5470951e  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: Amino Acid  
; STRANDEDNESS:  
; TOPOLOGY: Unknown  
US-08-127-904-15

Query Match 100.0%; Score 19; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 5  
US-08-612-785B-10  
; Sequence 10, Application US/08612785B  
; Patent No. 5854204  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.

GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: January 3, 2003, 07:42:56 Search time 35 Seconds

(without alignments)  
15.229 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 19

Sequence: 1 KLVF 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
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- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	4	18	AAW45956
2	19	100.0	4	21	AAV79936
3	19	100.0	4	22	AAW82637
4	19	100.0	4	22	AAW82635
5	19	100.0	4	22	AAW84879
6	19	100.0	4	22	AAW84847
7	19	100.0	4	23	AAU96815
8	19	100.0	4	23	AAU96823
9	19	100.0	4	23	AAU11653
10	19	100.0	4	23	AAU11661

11	19	100.0	5	16	AAW87922	Test peptide used
12	19	100.0	5	17	AAW02315	Beta-amyloid modul
13	19	100.0	5	18	AAW45933	Partial sequence o
14	19	100.0	5	18	AAW45950	Amyloid beta pepti
15	19	100.0	5	18	AAW45966	Peptide derived fr
16	19	100.0	5	20	AAW29089	A-beta-binding pep
17	19	100.0	5	20	AAW89367	Beta-amyloid pepti
18	19	100.0	5	21	AAV79937	Beta-amyloid recog
19	19	100.0	5	22	AAW82629	All-D peptide used
20	19	100.0	5	22	AAW82637	Residues 16-20 of
21	19	100.0	5	22	AAW62803	Antifibrillogenic
22	19	100.0	5	22	AAW67279	Antifibrillogenic
23	19	100.0	5	22	AAW48481	Transglutaminase 1
24	19	100.0	5	22	AAW48489	Amyloid targeting
25	19	100.0	5	23	AAW84801	Peptide #8, used a
26	19	100.0	5	23	AAU96817	Beta amyloid pepti
27	19	100.0	5	23	AAU96825	Beta-amyloid modul
28	19	100.0	5	23	AAU11655	Beta-amyloid modul
29	19	100.0	5	23	AAU11663	Amyloid beta pepti
30	19	100.0	5	23	AAW05158	A-beta-binding pep
31	19	100.0	5	23	AAW05183	A-beta-binding pep
32	19	100.0	6	17	AAW02331	Beta amyloid pepti
33	19	100.0	6	17	AAW02313	Beta-amyloid modul
34	19	100.0	6	17	AAW02314	Beta-amyloid modul
35	19	100.0	6	18	AAW45944	Amyloid beta pepti
36	19	100.0	6	18	AAW45945	Amyloid beta pepti
37	19	100.0	6	20	AAW29090	A-beta-binding pep
38	19	100.0	6	20	AAW29091	A-beta-binding pep
39	19	100.0	6	20	AAW89388	Beta-amyloid pepti
40	19	100.0	6	20	AAW89377	Beta-amyloid pepti
41	19	100.0	6	20	AAW89378	Beta-amyloid pepti
42	19	100.0	6	22	AAW82632	All-D peptide used
43	19	100.0	6	22	AAW82651	All-D peptide used
44	19	100.0	6	22	AAW82651	All-D peptide used
45	19	100.0	6	22	AAW82654	All-D peptide used

## ALIGNMENTS

RESULT 1  
AAW45956 standard; peptide; 4 AA.

AC AAW45956;  
DT 30-JUN-1998 (first entry)  
XX  
DE Amyloid beta peptide fragment.  
XX  
KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
XX postlorn emission tomography; PET; Down's syndrome; amyloidosis.  
XX  
OS Homo sapiens.  
XX  
PN MO9721728-A1.  
XX  
PD 19-JUN-1997.  
XX  
PF 09-DEC-1996; 96WO-SE01621.  
XX  
PR 29-DEC-1995; 95US-0009386.  
XX 12-DEC-1995; 95SE-0004467.  
XX  
BA (KARO-) KAROLINSKA INNOVATIONS AB.  
XX  
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;  
XX  
DR WPI; 1997-332723/30.  
XX  
PT Use of new and known peptide(s) for inhibition of polymerisation of  
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
PT Down's syndrome associated with amyloidosis.

XX Example 1; Figure 2B; 3lpp; English.

XX This sequence represents a fragment of the amyloid beta peptide. The

XX invention relates to the use of peptide compounds for inhibition of

XX polymerisation of amyloid beta peptide (ABP), as model substances for

XX synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a

XX tool for the identification of other organic compounds with similar

XX functional properties, or as ligands in positron emission tomography.

XX The peptides may be used in treatment of amyloidosis, especially in

XX treatment of Alzheimer's disease associated with Down's syndrome, for

XX treatment or prevention of hereditary cerebral haemorrhage with

XX amyloidosis (Dutch type) or for the prevention of fibril formation of

XX human amyloid protein. They can also be used for identifying other

XX molecules with similar properties and/or as ligands for detection of

XX amyloid deposits using e.g. positron emission tomography.

XX Sequence 4 AA;

Query Match 100.0%; Score 19; DB 18; Length 4;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVF 4

Db 1 KLVF 4

RESULT 2

AA79936

ID AA79936 standard; peptide; 4 AA.

AC AA79936;

DT 11-MAY-2000 (first entry)

DE Beta-amyloid recognition peptide SEQ ID NO:1.

XX Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;

XX Alzheimer's disease; neuroprotective; nontropic.

XX Homo sapiens

XX US6022859-A.

XX 08-FEB-2000.

XX 14-NOV-1997; 97US-0970833.

XX 15-NOV-1996; 96US-0030840.

XX (WISC.) WISCONSIN ALUMNI RES FOUND.

XX Murphy RM, Kiessling LU;

XX WPI; 2000-160387/14.

XX Beta-amyloid inhibitor useful for treating Alzheimer's disease -

XX Example; Column 7; 15pp; English.

XX The present invention describes a beta-amyloid inhibitor peptide.

XX Beta-amyloid inhibitors have neuroprotective and nontropic

XX properties. The inhibitor peptides are useful for the treatment of

XX Alzheimer's disease. The present sequence represents a beta-amyloid

XX recognition peptide used in the exemplification of present invention.

XX Sequence 4 AA;

Query Match 100.0%; Score 19; DB 21; Length 4;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KLVF 4

Db 1 KLVF 4

RESULT 3

AA82627

ID AA82627 standard; Peptide; 4 AA.

XX AA82627;

DT 02-OCT-2001 (first entry)

DE All-D peptide used in Alzheimer's disease vaccine.

XX Alzheimer's disease; amyloidosis; amyloid-related disease;

XX vaccine; therapy; antigen.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1.4

FT /note= "all D-form residues"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA01413.

XX 29-NOV-1999; 99US-0168594.

XX 28-NOV-2000; 2000US-0724842.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Hebert L, Kong X, Gervais F;

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's

XX disease, comprises administering antigenic all-D peptide, e.g. as

XX vaccine, which elicits production of antibodies to prevent

XX fibrillogenesis and associated cellular toxicity -

XX Disclosure; Page 11; 3lpp; English.

XX The present sequence is that of an all-D peptide suitable for

XX use for preparing vaccines for preventing or treating Alzheimer's

XX disease and other amyloid related disorders in humans. It is based

XX on a portion of amyloid-beta peptide (see AA82622), and may be

XX modified by removing or inserting 1 or more amino acid residues, or

XX by substituting 1 or more amino acid residues with other amino acid

XX residues or non-amino acid fragments. Vaccines of the invention

XX are produced using 'non-self' peptides synthesised from the

XX unnatural D-configuration amino acids to avoid the drawbacks of

XX 'self' proteins. The all-D peptides need not be aggregated to be

XX operative or immunogenic. They preferably interact with at

XX least 1 region of an amyloid protein, e.g. the beta-sheet region

XX or GAG-binding site region, the amyloid-beta peptide, or their

XX immunogenic fragments, protein conjugates, immunogenic derivative

XX peptides and immunogenic peptidomimetics. Examples include all-D

XX peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,

XX 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D

XX derivative peptides given in AA82623-64. The vaccine elicits a

XX preferential TH-2 or TH-1 response, preventing fibrillogenesis and

XX associated cellular toxicity. The amyloid related diseases may be

XX localised amyloidosis, e.g. diabetes type II, neurodegenerative

XX diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob

XX disease, scrapie, cerebral amyloid angiopathy, and prion protein

XX related disorders, or systemic amyloidosis associated with chronic

XX infection (e.g. tuberculosis) or chronic inflammation (e.g.

XX rheumatoid arthritis), familial Mediterranean fever (FMF) and

CC systemic amyloidosis found in long-term haemodialysis patients.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 19; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 1 KLVF 4  
 DB 1 KLVF 4

RESULT 4  
 AAB82635  
 ID AAB82635 standard; Peptide; 4 AA.  
 XX  
 NC AAB82635;  
 DT 02-OCT-2001 (first entry)  
 XX  
 DE All-D peptide used in Alzheimer's disease vaccine.  
 XX  
 KM Alzheimer's disease; amyloidosis; amyloid-related disease;  
 KM vaccine; therapy; antigen.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..4  
 FT Modified-site 6 /note= "all D-form residues"  
 FT Modified-site 6 /note= "C-terminal amide"  
 XX  
 PN WO200139796-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 29-NOV-2000; 2000WO-CA01413.  
 XX  
 PR 29-NOV-1999; 99US-0168594.  
 PR 28-NOV-2000; 2000US-0724842.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 PI Chalfour R, Hebert L, Kong X, Gervais F;  
 XX WPI; 2001-441458/47.  
 XX  
 DR  
 XX  
 PT Preventing/creating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, e.g. as  
 PT vaccine, which elicits production of antibodies to prevent  
 PT fibrillogenesis and associated cellular toxicity -  
 XX  
 PS Disclosure; Page 11; 31pp; English.  
 XX  
 XX The present sequence is that of an all-D peptide suitable for  
 CC use in preparing vaccines for preventing or treating Alzheimer's  
 CC disease and other amyloid related disorders in humans. It is based  
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be  
 CC modified by removing or inserting 1 or more amino acid residues, or  
 CC by substituting 1 or more amino acid residues with other amino acid  
 CC residues or non-amino acid fragments. Vaccines of the invention  
 CC are produced using 'non-self' peptides synthesised from the  
 CC unnatural D-configuration amino acids to avoid the drawbacks of  
 CC 'self' proteins. The all-D peptides need not be aggregated to be  
 CC operative or immunogenic. They preferably interact with at  
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region  
 CC or GAG-binding site region, the amyloid-beta peptide, or their  
 CC immunogenic fragments, protein conjugates, immunogenic derivative  
 CC peptides and immunogenic peptidomimetics. Examples include all-D  
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,  
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D

CC derivative peptides given in AAB82623-64. The vaccine elicits a  
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and  
 CC associated cellular toxicity. The amyloid related diseases may be  
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative  
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob  
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein  
 CC related disorders, or systemic amyloidosis associated with chronic  
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and  
 CC systemic amyloidosis found in long-term haemodialysis patients.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 19; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 1 KLVF 4  
 DB 1 KLVF 4

RESULT 5  
 AAB48479  
 ID AAB48479 standard; Peptide; 4 AA.  
 XX  
 AC AAB48479;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Antifibrillogenic peptide #6.  
 XX  
 KM Neotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KM cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KM Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200068263-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PF 04-MAY-2000; 2000WO-CA00515.  
 XX  
 PR 05-MAY-1999; 99US-0132592.  
 XX  
 PA (NEUR-) NEUROCHEM INC.  
 XX  
 PI Chalfour R, Gervais F, Gupta A;  
 XX WPI; 2001-031852/04.  
 XX  
 DR  
 XX  
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic -  
 XX  
 PS Claim 7; Page 25; 46pp; English.  
 XX  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are  
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's  
 CC disease. Peptides AAB48474-B48496 were identified from the  
 CC glycosaminoglycan binding region and the prot-prot interaction region of  
 CC the human amyloid protein.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 19; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4

Db 1 KLVF 4

RESULT 6  
AAB48487

ID AAB48487 standard; Peptide; 4 AA.  
AC AAB48487;  
XX  
XX 02-MAR-2001 (first entry)  
XX  
XX Antifibrillogenic peptide #14.  
XX  
XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
KW Alzheimer's disease.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 4  
FT /note= "C-terminal amide"  
XX  
XX WO200068263-A2.  
XX  
XX 16-NOV-2000.  
XX  
XX 04-MAY-2000; 2000WO-CA00515.  
XX  
XX 05-MAY-1999; 99US-0132592.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Chalifour R, Gervais F, Gupta A;  
XX WPI; 2001-031852/04.  
XX  
XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
XX cytoprotection for treating amyloidosis disorders, comprises a peptide,  
XX its isomer or peptidomimetic  
XX  
XX Claim 7; Page 25; 46pp; English.  
XX  
XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
XX for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
XX AAB48474-B48496 cause the breakdown of amyloid deposits and are  
XX therefore useful for treating amyloidosis disorders such as Alzheimer's  
XX disease. Peptides AAB48474-B48496 were identified from the  
XX glycosaminoglycan binding region and the prot-prot interaction region of  
XX the human amyloid protein.

Sequence 4 AA;  
Query Match 100.0%; Score 19; DB 22; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 7  
AAU96815

ID AAU96815 standard; peptide; 4 AA.  
XX  
XX AAU96815;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX Amyloid targeting peptide #5.

KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
KW transmissible cerebral amyloidosis; transmissible virus dementia;  
KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;  
KW bovine spongiform encephalopathy; inflammation associated amyloid;  
KW primary amyloidosis; feline spongiform encephalopathy;  
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
KW dialysis-related amyloidosis; light chain-related amyloidosis;  
KW cerebral amyloid angiopathy.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..4  
FT /note= "Preferably D-form residue"  
XX  
XX WO200207781-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 25-JUL-2001; 2001WO-CA01071.  
XX  
XX 25-JUL-2000; 2000US-220808P.  
XX  
XX 24-JUL-2001; 2001US-0915092.  
XX  
XX (NEUR-) NEUROCHEM INC.  
XX  
XX Gervais F, Kong X, Chalifour R, Migneault D;  
XX WPI; 2002-371447/40.  
XX  
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid  
XX plaques and/or for the treatment of amyloidosis disorders  
XX  
XX Claim 49; Page 21; 57pp; English.  
XX  
XX The invention relates to an amyloid-targeting imaging agent comprising  
XX an amyloid targeting moiety, a linker moiety and a labelling moiety.  
XX The agent is of general formula A<sub>1</sub>-<sub>(A<sub>1</sub>)<sub>n</sub></sub>-<sub>(A<sub>2</sub>)<sub>m</sub></sub>-<sub>(A<sub>3</sub>)<sub>k</sub></sub>-<sub>(A<sub>4</sub>)<sub>p</sub></sub> where  
XX z = 0 - 1; A<sub>1</sub> = an amyloid targeting moiety; A<sub>2</sub> = a linker  
XX moiety; and A<sub>3</sub> = a labelling moiety. Also included are imaging  
XX amyloid deposition or diagnosing an amyloid-related condition in a  
XX patient involving administering (I) to the patient, and ultrasound  
XX imaging (I) in the patient to determine the presence of amyloid or  
XX amyloid-related condition; and a kit for preparing a radiopharmaceutical  
XX preparation comprising (I), a reducing agent, a buffering agent, a  
XX transchelating agent, and instructions for the preparation and use of the  
XX radiopharmaceutical in the imaging of amyloid or an amyloid-related  
XX condition. The agents are used for imaging amyloid deposition and for  
XX diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease  
XX (CJD), Kuru, transmissible cerebral amyloidosis (transmissible virus  
XX dementias), familial CJD, scrapie, transmissible mink encephalopathy,  
XX type II diabetes, primary amyloidosis, feline spongiform encephalopathy,  
XX bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,  
XX non-transmissible cerebral amyloidosis, Alzheimer's disease,  
XX prion-mediated diseases, dialysis-related amyloidosis, light  
XX chain-related amyloidosis, cerebral amyloid angiopathy. The agents are  
XX capable of crossing the blood-brain barrier and are capable of binding  
XX specifically to amyloid plaques. The present sequence is a peptide  
XX forming the amyloid targeting moiety of the agent of the invention.

Sequence 4 AA;  
Query Match 100.0%; Score 19; DB 23; Length 4;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 8  
AAU96823

ID AAU96823 standard; peptide; 4 AA.  
AC AAU96823;  
AT 30-JUL-2002 (first entry)  
XX Amyloid targeting peptide #13.  
XX  
KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;  
transmissible cerebral amyloidosis; transmissible virus dementia;  
Kw bovine spongiform encephalopathy; BSE; type II diabetes;  
KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;  
amyloid plaques and/or for the treatment of amyloidosis disorders -  
cerebral amyloid angiopathy.

	Key	Location/Qualifiers
OS MISC-difference	1..4	/note= "Preferably D-form residue"
FT Modified-site	4	/note= "Phe is amidated"
PN WO200207781-A2.		
PD 31-JAN-2002.		
PF 25-JUL-2001; 2001WO-CN01071.		
PR 25-JUL-2000; 2000US-220808P.		
PA 24-JUL-2001; 2001US-0915092.		
(NEUR-) NEUROCHEM INC.		
Gervais F, Kong X, Chalifour R, Migneault D;		
WPI; 2002-371447/40.		

New amyloid-targeting imaging agents useful for in vivo imaging amyloid plaques and/or for the treatment of amyloidosis disorders -

Claim 49, Page 21, 57pp, English.

The invention relates to an amyloid-targeting imaging agent comprising an amyloid targeting moiety, a linker moiety and a labelling moiety. The agent is of general formula A-t(A<sub>1</sub>n<sub>k</sub>)z-A<sub>1</sub>a<sub>b</sub> (I) where z = 0 - 1; A<sub>t</sub> = an amyloid targeting moiety; A<sub>1</sub>n<sub>k</sub> = a linker moiety; and A<sub>1</sub>a<sub>b</sub> = a labelling moiety. Also included are imaging amyloid deposit or diagnosing an amyloid-related condition in a patient involving administering (I) to the patient, and ultrasound imaging (I) in the patient to determine the presence of amyloid or amyloid-related condition; and a kit for preparing a radiopharmaceutical preparation comprising (I), a reducing agent, a buffering agent, a transchelating agent, and instructions for the preparation and use of the radiopharmaceutical in the imaging of amyloid or an amyloid-related condition. The agents are used for imaging amyloid deposition and for diagnosing an amyloid related condition e.g. Creutzfeldt-Jacob disease (CJD), kuru, transmissible cerebral amyloidoses (transmissible virus dementia), familial CJD, scrapie, transmissible mink encephalopathy, type I diabetes, primary amyloidosis, feline spongiform encephalitis, non-transmissible cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy. The agents are capable of crossing the blood-brain barrier and are capable of binding specifically to amyloid plaques. The present sequence is a peptide forming the amyloid targeting moiety of the agent of the invention.

Sequence 4 AA.

Query Match 100.0%; Score 19; DB 23; Length 4;

OY		1 KLVF 4       		Best Local Similarity 100.0%; Pred. No. 7.8e+05;	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db		1 KLVF 4			
RESULT 9					
AU011653	ID	AU011653 standard; Peptide; 4 AA.			
XX	AC	AAU1653;			
XX	DT	09-APR-2002 (first entry)			
XX	DE	Peptide #6, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.			
XX	KW	Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy; CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease; cerebral haemorrhage; amyloidosis; haemorrhagic stroke.			
OS	Synthetic.				
PV	WO200185093-A2.				
PD	15-NOV-2001.				
PP	22-DEC-2000; 2000WO-IB02078.				
PR	23-DEC-1999; 99US-171877P.				
PA	(NEUR-) NEUROCHEM INC.				
PI	Green AM, Gervais F;				
DR	WPI; 2002-075222/10.				
PT	Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's disease comprises contacting blood vessel wall cell with amyloid-beta 40 inhibitor -				
PS	Disclosure; Page 10; 68pp; English.				
CC	The present invention relates to a new method of inhibiting cerebral amyloid angiopathy. The new method of the invention involves contacting a blood vessel wall cell with an amyloid-beta40 inhibitor. The invention can be used for treating disease states characterised by cerebral amyloid angiopathy, particularly Alzheimer's disease, hereditary cerebral haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke. The present sequence represents one of a group of peptides (AU011648-AU011669, AU011910 & AU011911) that were used in the invention as a carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor was used in the invention to treat a disease state characterised by cerebral amyloid angiopathy (CAA).				
CC	Sequence 4 AA;				
CC	Query Match	100.0%; Score 19; DB 23; Length 4;			
CC	Best Local Similarity 100.0%; Pred. No. 7.8e+05;				
CC	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY		1 KLVF 4       			
Db		1 KLVF 4			
RESULT 10					
AU011661	ID	AU011661 standard; Peptide; 4 AA.			
AC	AAU1661;				
XX					

DT 09-APR-2002 (first entry)  
 XX Peptide #14, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 DE Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;  
 XX CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;  
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.  
 KW  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 4  
 FT /note= "C-terminal amide"  
 XX  
 XX WO200185093-A2.  
 XX  
 XX 15-NOV-2001.  
 XX  
 XX 22-DEC-2000; 2000WO-IB02078.  
 XX  
 XX 23-DEC-1999; 99US-171877P.  
 XX  
 XX (NEUR-) NEUROCHEM INC.  
 XX  
 XX Green AM, Gervais F;  
 PI  
 XX WPI; 2002-075222/10.  
 DR  
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g.  
 PT Alzheimer's disease comprises contacting blood vessel wall cell with  
 PT amyloid-beta 40 inhibitor -  
 XX  
 XX Disclosure; Page 10; 68pp; English.  
 PS  
 XX The present invention relates to a new method of inhibiting cerebral  
 CC amyloid angiopathy. The new method of the invention involves contacting  
 CC a blood vessel wall cell with an amyloid-beta40 inhibitor. The invention  
 CC can be used for treating disease states characterised by cerebral  
 CC amyloid angiopathy, particularly Alzheimer's disease, hereditary  
 CC cerebral haemorrhage with amyloidosis of the Dutch type and  
 CC cerebral haemorrhagic stroke. The present sequence represents one of a group  
 CC of peptides (AAU11648-AAU11669, AAU11910 & AAU11911) that were used in  
 CC the invention as a carrier for the amyloid-beta40 (Abeta40) inhibitor.  
 CC The Abeta40 inhibitor was used in the invention to treat a disease  
 CC state characterised by cerebral amyloid angiopathy (CAA).  
 XX  
 XX Sequence 4 AA;  
 SQ  
 Query Match 100.0%; Score 19; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB ||||  
 1 KLVP 4  
 RESULT 11  
 AAR87922  
 ID AAR87922 standard; peptide; 5 AA.  
 XX  
 AC AAR87922;  
 XX  
 XX 01-MAR-1996 (first entry)  
 DT  
 XX Test peptide used in study of antagonism of amyloid beta protein.  
 DE  
 XX amnesia; amyloid beta; Alzheimer's disease.  
 KW  
 XX Synthetic.  
 OS  
 XX W09508999-A1.  
 PN  
 XX

PD 06-APR-1995.  
 XX  
 XX 16-SEP-1994; 94WO-US10475.  
 XX  
 XX 29-SEP-1993; 93US-0127904.  
 XX  
 XX (CITY ) CITY OF HOPE.  
 PA  
 XX Roberts E;  
 PI  
 XX WPI; 1995-147244/19.  
 DR  
 XX New peptide(s) which block binding of amyloid beta protein - used  
 PT for antagonising the amnesic effects of amyloid beta protein,  
 PT partic. in Alzheimer's disease  
 XX  
 XX Disclosure; Page 9; 27pp; English.  
 PS  
 XX The invention relates to three new peptides which block the amnesic  
 CC effects of amyloid beta protein and which can be used to ameliorate  
 CC amnesia and other neurotoxicity in Alzheimer's disease caused by  
 CC deposition of this protein. The peptides themselves are not amnesic or  
 CC memory-enhancing. The new peptides are described in AAR87912, AAR87913  
 CC and AAR87914.  
 CC The present sequence is an additional peptide tested in the process  
 CC but found not to be active.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 100.0%; Score 19; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVP 4  
 DB ||||  
 1 KLVP 4  
 RESULT 12  
 AAW02315  
 ID AAW02315 standard; peptide; 5 AA.  
 XX  
 AC AAW02315;  
 XX  
 XX 02-MAY-1997 (first entry)  
 DT  
 XX Beta-amyloid modulator peptide #6.  
 DE  
 XX Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;  
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;  
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;  
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;  
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;  
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9628471-A1.  
 PN  
 XX 19-SEP-1996.  
 PD  
 XX 14-MAR-1996; 96WO-US03492.  
 XX  
 XX 27-OCT-1995; 95US-0548998.  
 PR  
 XX 14-MAR-1995; 95US-0404831.  
 PR  
 XX 07-JUN-1995; 95US-0475579.  
 PR  
 XX (PHAR-) PHARM PEPTIDES INC.  
 PA  
 XX Benjamin H, Chin J, Findeis MA, Garnick MB, Geffer ML;  
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;



XX WPI; 1996-433762/43.  
XX  
XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic  
PT protein coupled (in)directly to at least 1 modifying gp., useful in  
PT treatment of Alzheimer's disease  
XX  
PS Claim 16; Page 91; 106pp; English.  
XX  
XX AAM02310-W02332 represent the peptide portions of the beta-amyloid  
CC modulator compounds of the invention. Beta-amyloid peptide is a 4  
CC kilodalton peptide that is the major protein component of amyloid  
CC plaques. Amyloid plaques are present both in the brain lesions, and in  
CC the walls of cerebral blood vessels in Alzheimer's disease patients.  
CC The amyloid modulators of the invention comprise an amyloidogenic protein  
CC or peptide (such as this sequence) coupled directly or indirectly to at  
CC least one modifying group. The modifying group is preferably a cyclic,  
CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a  
CC biotin containing group, or a fluorescein containing group. These  
CC compounds then modulate the aggregation of these sequences to natural  
CC amyloid proteins or peptides when contacted with the natural  
CC amyloidogenic proteins or peptides. The modulator compounds can be used  
CC in the treatment of disorders associated with amyloidosis, such as  
CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,  
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,  
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset  
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid  
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage  
CC and other types of amyloidosis. The modulators are also useful for the  
CC treatment of disorders associated with beta-amyloidosis, especially  
CC Alzheimer's disease.  
XX  
XX Sequence 5 AA;  
SQ  
Query Match 100.0%; Score 19; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
DB 1 KLVF 4  
RESULT 13  
AAM45933  
ID AAM45933 standard; peptide; 5 AA.  
XX  
XX AAM45933;  
AC  
XX 08-JUL-1998 (first entry)  
DT  
XX  
XX Partial sequence of amyloid beta peptide critical for its polymerisation.  
DE  
XX  
XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
KM positron emission tomography; PET; Down's syndrome; amyloidosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W09721728-A1.  
PN  
XX  
XX 19-JUN-1997.  
PD  
XX  
XX 09-DEC-1996; 96WO-SE01621.  
PF  
XX  
XX 29-DEC-1995; 95US-0009386.  
PR  
XX 12-DEC-1995; 95SE-0004467.  
PR  
XX (KARO-) KAROLINSKA INNOVATIONS AB.  
PA  
XX  
XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;  
PI WPI; 1997-332723/30.  
XX

PT Use of new and known peptide(s) for inhibition of polymerisation of  
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
PT Down's syndrome associated with amyloidosis.  
XX  
XX Example 5; Page 14; 31pp; English.  
XX  
XX This is a partial sequence of the amyloid beta peptide which is critical  
CC for its polymerisation. The invention relates to the use of peptide  
CC compounds for inhibition of polymerisation of amyloid beta peptide  
CC (ABP), as model substances for synthesis of ABP-ligands for inhibition  
CC of polymerisation of ABP, as a tool for the identification of other  
CC organic compounds with similar functional properties, or as ligands in  
CC positron emission tomography. The peptides may be used in treatment of  
CC amyloidosis, especially in treatment of Alzheimer's disease associated  
CC with amyloidosis, for treatment or prevention of dementia in patients with  
CC Down's syndrome, for treatment or prevention of hereditary cerebral  
CC haemorrhage with amyloidosis (bitch type) or for the prevention of  
CC fibril formation of human amyloid protein. They can also be used for  
CC identifying other molecules with similar properties and/or as ligands  
CC for detection of amyloid deposits using e.g. positron emission  
CC tomography.  
XX  
XX Sequence 5 AA;  
SQ  
Query Match 100.0%; Score 19; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
DB 1 KLVF 4  
RESULT 14  
AAM45950  
ID AAM45950 standard; peptide; 5 AA.  
XX  
XX AAM45950;  
AC  
XX  
XX 30-JUN-1998 (first entry)  
DT  
XX  
XX Amyloid beta peptide fragment.  
DE  
XX  
XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
KM positron emission tomography; PET; Down's syndrome; amyloidosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W09721728-A1.  
PN  
XX  
XX 19-JUN-1997.  
PD  
XX  
XX 09-DEC-1996; 96WO-SE01621.  
PF  
XX  
XX 29-DEC-1995; 95US-0009386.  
PR  
XX 12-DEC-1995; 95SE-0004467.  
PR  
XX (KARO-) KAROLINSKA INNOVATIONS AB.  
PA  
XX  
XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;  
PI WPI; 1997-332723/30.  
XX  
XX Use of new and known peptide(s) for inhibition of polymerisation of  
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
PT Down's syndrome associated with amyloidosis.  
XX  
XX Example 1; Figure 2B; 31pp; English.  
XX  
XX This sequence represents a fragment of the amyloid beta peptide. The  
CC invention relates to the use of peptide compounds for inhibition of  
CC polymerisation of amyloid beta peptide (ABP), as model substances for  
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a

CC tool for the identification of other organic compounds with similar  
 CC functional properties, or as ligands in positron emission tomography.  
 CC The peptides may be used in treatment of amyloidosis, especially in  
 CC treatment of Alzheimer's disease associated with amyloidosis, for  
 CC treatment or prevention of demens in patients with Down's syndrome, for  
 CC treatment or prevention of hereditary cerebral haemorrhage with  
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of  
 CC human amyloid protein. They can also be used for identifying other  
 CC molecules with similar properties and/or as ligands for detection of  
 CC amyloid deposits using e.g. positron emission tomography.

XX Sequence 5 AA;

Query Match 100.0%; Score 19; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 ||||  
 Db 2 KLVF 5

# RESULT 15

AAW45966  
 ID AAW45966 standard; peptide; 5 AA.

XX AC AAW45966;

XX 30-JUN-1998 (first entry)

XX Peptide derived from amyloid beta peptide fragment.

XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;  
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.

XX Homo sapiens.

XX Synthetic.

XX WO9721728-A1.

XX 19-JUN-1997.

XX 09-DEC-1996; 96WO-SE01621.

XX 29-DEC-1995; 95US-0009386.

XX 12-DEC-1995; 95SE-0004467.

XX (KARO-) KAROLINSKA INNOVATIONS AB.

XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

XX WPI; 1997-332723/30.

XX Use of new and known peptide(s) for inhibition of polymerisation of  
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or  
 PT Down's syndrome associated with amyloidosis.

XX Example 1; Figure 2C; 31pp; English.

XX Sequences AAW45962-6 represent a fragment of the amyloid beta peptide  
 CC KLVFF with an amino acid residue replaced with alanine. The invention  
 CC relates to the use of peptide compounds for inhibition of polymerisation  
 CC of amyloid beta peptide (ABP), as model substances for synthesis of  
 CC ABP-ligands for inhibition of polymerisation of ABP, as a tool for the  
 CC identification of other organic compounds with similar functional  
 CC properties, or as ligands in positron emission tomography. The peptides  
 CC may be used in treatment of amyloidosis, especially in treatment of  
 CC Alzheimer's disease associated with amyloidosis, for treatment or  
 CC prevention of demens in patients with Down's syndrome, for treatment or  
 CC prevention of hereditary cerebral haemorrhage with amyloidosis (Dutch  
 CC type) or for the prevention of fibril formation of human amyloid  
 CC protein. They can also be used for identifying other molecules with  
 CC similar properties and/or as ligands for detection of amyloid deposits

CC using e.g. positron emission tomography.

XX Sequence 5 AA;

Query Match 100.0%; Score 19; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4

||||

Db 1 KLVF 4

Search completed: January 3, 2003, 07:44:00  
 Job time : 36 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:42:57 ; Search time 15 Seconds  
(without alignments)  
25.636 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 19  
Sequence: 1 KLVP 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	16	2 F41299	T-cell receptor al
2	19	100.0	26	2 G32502	T-cell receptor de
3	19	100.0	29	2 C47719	T-cell receptor al
4	19	100.0	30	2 B31461	T-cell receptor de
5	19	100.0	31	2 B31461	T-cell receptor de
6	19	100.0	32	2 D32502	T-cell receptor de
7	19	100.0	32	2 A32502	T-cell receptor de
8	19	100.0	32	2 D31461	T-cell receptor de
9	19	100.0	32	2 B32540	T-cell receptor de
10	19	100.0	33	2 B32502	T-cell receptor de
11	19	100.0	33	2 I31461	T-cell receptor de
12	19	100.0	33	2 A31461	T-cell receptor de
13	19	100.0	33	2 B31461	T-cell receptor de
14	19	100.0	33	2 S23094	beta-amyloid prote
15	19	100.0	34	2 I32502	T-cell receptor de
16	19	100.0	34	2 C31461	T-cell receptor de
17	19	100.0	34	2 H31461	T-cell receptor de
18	19	100.0	36	2 H32502	T-cell receptor de
19	19	100.0	36	2 A32540	T-cell receptor de
20	19	100.0	36	2 C32502	T-cell receptor de
21	19	100.0	42	2 FN0512	beta-amyloid prote
22	19	100.0	47	2 PC4133	hypothetical 47 pr
23	19	100.0	53	2 PS0009	glycophorin A1ab1b pr
24	19	100.0	57	2 B60045	Alzheimer's diseas
25	19	100.0	57	2 F60045	Alzheimer's diseas
26	19	100.0	57	2 G60045	Alzheimer's diseas
27	19	100.0	57	2 D60045	Alzheimer's diseas
28	19	100.0	57	2 A60045	Alzheimer's diseas
29	19	100.0	57	2 B60045	Alzheimer's diseas

30	19	100.0	57	2 D97742	hypothetical prote
31	19	100.0	67	2 B97758	hypothetical prote
32	19	100.0	69	2 B33979	peptidyl-dipectida
33	19	100.0	69	2 T46201	protein translocat
34	19	100.0	71	2 AB2884	hypothetical prote
35	19	100.0	72	2 S28793	major merozoite su
36	19	100.0	73	2 A38883	rab protein Rab6 -
37	19	100.0	75	2 S35774	T-cell receptor al
38	19	100.0	78	2 B84305	hypothetical prote
39	19	100.0	79	2 C97829	hypothetical prote
40	19	100.0	81	2 H71614	protein translocat
41	19	100.0	82	2 PQ0438	Alzheimer's diseas
42	19	100.0	83	2 AD2896	hypothetical prote
43	19	100.0	84	2 AC3376	hypothetical prote
44	19	100.0	86	1 C64322	ribosomal protein
45	19	100.0	86	2 B44530	T-cell receptor al

#### ALIGNMENTS

##### RESULT 1

F41299 T-cell receptor alpha chain precursor U region (37) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 28-May-1992 #sequence\_revision 28-May-1992 #ext\_change 05-Nov-1999  
C/Accession: F41299  
R/Jematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Banwarth, W.; Lanchbury, J.; Panayi, G.; Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991  
A/Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumat.  
A/Reference number: A41299; PMID:92020887; PMID:1656449  
A/Accession: F41299  
A/Status: Preliminary  
A/Molecule type: mRNA  
A/Residues: 1-16 <UM>  
A/Cross-references: GB:S57448; NID:G236328; PIDN:ABJ1961.1; PID:G236329  
C/Keywords: T-cell receptor

##### Query Match

Best Local Similarity 100.0%; Score 19; DB 2; Length 16;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
Db 3 KLVP 6

##### RESULT 2

G32502 T-cell receptor delta chain MLC6, spleen - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #ext\_change 30-May-1997  
C/Accession: G32502  
R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.; Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989  
A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.  
A/Reference number: A31461; PMID:89128840; PMID:2783779  
A/Accession: G32502  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-26 <LAC>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

##### Query Match

Best Local Similarity 100.0%; Score 19; DB 2; Length 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
Db 13 KLVP 16

```

RESULT 3
C47719
T-cell receptor alpha chain (V-J region, CD4+ clone DDL1, house-dust-mite-reactive) - hu
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C/Accession: C47719
R/Wedderburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993
A/Title: In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell
A/Reference number: A47719; MUID:93376774; PMID:8367485
A/Accession: C47719
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-29 <WEB>
A/Note: sequence extracted from NCBI backbone (NCBIN:137814, NCBIIP:137820)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 12 KLVF 15

RESULT 4
E31461
T-cell receptor delta chain BDN9, thymus - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C/Accession: E31461
R/Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A/Reference number: A31461; MUID:89128840; PMID:2783779
A/Accession: E31461
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: mRNA
A/Residues: 1-30 <LAC>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 17 KLVF 20

RESULT 5
F31461
T-cell receptor delta chain BDN10, thymus - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C/Accession: F31461
R/Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A/Reference number: A31461; MUID:89128840; PMID:2783779
A/Accession: F31461
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-31 <LAC>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KLVF 4
DB 18 KLVF 21

RESULT 6
D32502
T-cell receptor delta chain CDN35, thymus - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C/Accession: D32502
R/Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A/Reference number: A31461; MUID:89128840; PMID:2783779
A/Accession: D32502
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-32 <LAC>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 19 KLVF 22

RESULT 7
A32502
T-cell receptor delta chain CDN26, thymus - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C/Accession: A32502
R/Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A/Reference number: A31461; MUID:89128840; PMID:2783779
A/Accession: A32502
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-32 <LAC>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 19 KLVF 22

RESULT 8
D31461
T-cell receptor delta chain BDN7, thymus - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C/Accession: D31461
R/Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A/Reference number: A31461; MUID:89128840; PMID:2783779
A/Accession: D31461
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-32 <LAC>
C/Superfamily: immunoglobulin V region; immunoglobulin homology

```

C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
DB 19 KLVF 22

RESULT 9

B32540 T-cell receptor delta chain, VDJ region (clone MLC24) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: B32540; B32502

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: B32540

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

A/Experimental source: clone MLC24 (spleen)

A/Accession: B32502

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

A/Experimental source: clone CDN28 (thymus)

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
DB 20 KLVF 23

RESULT 10

E32502

T-cell receptor delta chain MLC2, spleen - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: B32502

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: B32502

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
DB 20 KLVF 23

RESULT 11

I31461

T-cell receptor delta chain CDN15, thymus - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: I31461

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: I31461

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
DB 20 KLVF 23

RESULT 12

A31461

T-cell receptor delta chain BDN1, thymus - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: A31461

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: A31461

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
DB 20 KLVF 23

RESULT 13

B31461

T-cell receptor delta chain BDN3, thymus - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: B31461

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: B31461

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
DB 20 KLVF 23

RESULT 14  
S23094  
beta-amyloid protein precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C;Accession: S23094  
R;Kojima, S.; Omori, M.  
FEBS Lett. 304, 57-60, 1992  
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
A;Reference number: S23094; MUID:92316198; PMID:1618299  
A;Accession: S23094  
A;Molecule type: protein  
A;Residues: 1-33 <KOU>  
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 100.0%; Score 19; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KLVF 4  
Db 21 KLVF 24

RESULT 15  
I32502  
T-cell receptor delta chain MLC17, spleen - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997  
C;Accession: I32502  
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989  
A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.  
A;Reference number: A31461; MUID:89128840; PMID:2783779  
A;Accession: I32502  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-34 <LAC>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 100.0%; Score 19; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KLVF 4  
Db 21 KLVF 24

Search completed: January 3, 2003, 07:44:58  
Job time : 16 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2003, 07:42:56 ; Search time 11 Seconds  
(without alignments)  
15.082 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 19  
Sequence: 1 KLVF 4

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt.40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	57	A4_PIG	Q29023 sus scrofa
2	19	100.0	57	A4_URSWA	Q29149 ursus marit
3	19	100.0	58	A4_CANFA	Q28280 canis fami1
4	19	100.0	58	A4_RABIT	Q28748 cyclocolagus
5	19	100.0	58	A4_SHEEP	Q28757 ovis aries
6	19	100.0	59	A4_BOVIN	Q28053 bos taurus
7	19	100.0	86	R123_METUA	P54016 methanococc
8	19	100.0	91	P909_METUA	Q58319 methanococc
9	19	100.0	94	SPC1_YEAST	P46965 saccharomyc
10	19	100.0	95	PSC3_RAT	P02780 rattus norv
11	19	100.0	109	VNS2_CVHM	P15774 bovine corv
12	19	100.0	109	VNS2_CVHOC	Q04853 human corv
13	19	100.0	110	YCX1_CHLY	P05720 chlorella p
14	19	100.0	118	FCOLB_HAEIN	P43662 haemophilus
15	19	100.0	121	R22B_YEAST	P56328 saccharomyc
16	19	100.0	122	FCOLB_ECOLI	P31055 escherichia
17	19	100.0	127	CV2_RHOVI	P00083 rhodospseud
18	19	100.0	139	FABZ_STRPY	P58175 streptococc
19	19	100.0	140	FABZ_STRPN	Q97bc0 streptococc
20	19	100.0	144	FAZ2_LACIA	Q96hf4 lactococcus
21	19	100.0	146	RL13_MYCOE	P4657 mycoplasma
22	19	100.0	152	M165_ARATH	Q96717 arabidopsis
23	19	100.0	153	NUSB_FUSNN	Q96711 fusobacteri
24	19	100.0	156	SPRT_HAETN	P44139 haemophilus
25	19	100.0	162	FIGA_AGRYS	Q43339 agrobacteri
26	19	100.0	164	RL10_HELPJ	Q96k22 helicobacte
27	19	100.0	164	BA1E_EUBSP	P56036 helicobacte
28	19	100.0	166	BA1E_EUBSP	P19412 eubacterium
29	19	100.0	166	PMPA_CANBO	P14292 candida boi
30	19	100.0	169	YBGA_ECOLI	P24252 escherichia
31	19	100.0	176	VGB_CVFE3	P33467 feline ente
32	19	100.0	180	YAGL_BOVIN	Q96887 bos taurus
33	19	100.0	181	ITRB_BOVIN	P01071 glycine max

34	19	100.0	186	1	ATPD_CYAPA	P48082 cyanophora
35	19	100.0	190	1	YBAY_ECOLI	P77717 escherichia
36	19	100.0	191	1	TERE_ALCSP	P18782 alcaligenes
37	19	100.0	191	1	TERE_SERMA	Q52358 serratia ma
38	19	100.0	191	1	Y611_METUA	Q58028 methanococc
39	19	100.0	193	1	DYR_BPT4	P04382 bacterioph
40	19	100.0	193	1	SARI_CAEEL	Q23445 caenorhabdl
41	19	100.0	194	1	YD16_HAEIN	P44159 haemophilus
42	19	100.0	198	1	SARA_HUMAN	Q9nr31 homo sapien
43	19	100.0	198	1	SARA_MOUSE	P36536 mus musculu
44	19	100.0	198	1	SARP_HUMAN	Q9y6b6 homo sapien
45	19	100.0	198	1	SCP2_BACSU	P81100 bacillus su

## ALIGNMENTS

RESULT 1  
A4\_PIG  
ID A4\_PIG STANDARD; PRT; 57 AA.

AC Q25023;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-ApP) (A-beta)] (Fragment).  
GN APP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP TISSUE=Brain;  
RS SEQUENCE FROM N.A.

RC MEDLINE=92017079; PubMed=1656157;  
RA Uchmstone E.W., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC -----

DR EMBL; X56127; CAA39592.1; -.  
DR HSBP; P05067; IBA4.  
DR InterPro: IPR001868; A4 APP.  
DR InterPro: IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4 INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neurope; Transmembrane.  
FT CHAIN 1 48  
FT DOMAIN <1 33  
FT TRANSMEM 34 57  
FT NON\_TER 57  
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;

Query Match 100.0%; Score 19; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 KLVF 4
Db      21 KLVF 24

RESULT 2
A4_URSWA
ID      A4_URSWA      STANDARD;      PRT;      57 AA.
AC      Q29149;
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
OS      Ursus maritimus (Polar bear) (Thalarchos maritimus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX      NCBI_TaxID=29073;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56128; CAA39593.1; -.
DR      HSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1      1
FT      CHAIN      7      49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1      34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      35      58      POTENTIAL.
FT      NON_TER      58      58
FT      SEQUENCE      57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match      100.0%; Score 19; DB 1; Length 57;
Best Local Similarity      100.0%; Pred. No. 95;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 KLVF 4
Db      21 KLVF 24

RESULT 3
A4_CANFA
ID      A4_CANFA      STANDARD;      PRT;      58 AA.
AC      Q28280;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56128; CAA39593.1; -.
DR      HSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1      1
FT      CHAIN      6      48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1      33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34      57      POTENTIAL.
FT      NON_TER      57      57
FT      SEQUENCE      57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match      100.0%; Score 19; DB 1; Length 57;
Best Local Similarity      100.0%; Pred. No. 95;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 KLVF 4
Db      21 KLVF 24

RESULT 4
A4_RABIT
ID      A4_RABIT      STANDARD;      PRT;      58 AA.
AC      Q28748;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56125; CAA39590.1; -.
DR      HSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1      1
FT      CHAIN      7      49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1      34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      35      58      POTENTIAL.
FT      NON_TER      58      58
FT      SEQUENCE      58 AA; 6285 MW; 8469D489A2E12DFA CRC64;

Query Match      100.0%; Score 19; DB 1; Length 58;
Best Local Similarity      100.0%; Pred. No. 96;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 KLVF 4
Db      22 KLVF 25

RESULT 4
A4_RABIT
ID      A4_RABIT      STANDARD;      PRT;      58 AA.
AC      Q28748;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56125; CAA39590.1; -.
DR      HSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      InterPro; IPR001255; Beta-APP.
DR      Pfam; PF03494; Beta-APP; 1.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1      1
FT      CHAIN      7      49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1      34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      35      58      POTENTIAL.
FT      NON_TER      58      58
FT      SEQUENCE      58 AA; 6285 MW; 8469D489A2E12DFA CRC64;

Query Match      100.0%; Score 19; DB 1; Length 58;
Best Local Similarity      100.0%; Pred. No. 96;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 KLVF 4
Db      22 KLVF 25

```



RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X56129; CAA39594.1; -.  
 DR HSSP; P05067; IBA4.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurope; Transmembrane.  
 FT NON TER 1  
 FT CHAIN 1  
 FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 58 58 POTENTIAL.  
 FT NON TER 58  
 FT CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;  
 Query Match 100.0%; Score 19; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 21 KLVF 24  
 RESULT 5  
 A4\_SHEEP STANDARD; PRT; 56 AA.  
 ID A4\_SHEEP  
 AC Q28757;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).  
 GN APP.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RX MEDLINE=92017079; PubMed=1656157;  
 RC TISSUE=Heart;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -----

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 CC -----  
 DR EMBL; X56130; CAA39595.1; -.  
 DR HSSP; P05067; IBA4.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurope; Transmembrane.  
 FT NON TER 1  
 FT CHAIN 1  
 FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 58 58 POTENTIAL.  
 FT NON TER 58  
 FT CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;  
 Query Match 100.0%; Score 19; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 21 KLVF 24  
 RESULT 6  
 A4\_BOVIN STANDARD; PRT; 59 AA.  
 ID A4\_BOVIN  
 AC Q28053;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).  
 GN APP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RX MEDLINE=92017079; PubMed=1656157;  
 RC TISSUE=Brain;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X56124; CAA39589.1; -.  
 DR EMBL; X56126; CAA39591.1; -.

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DR HSP: P05067; 1BA4.
DR InterPro; IPR001868; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 19; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 22 KLVF 25

RESULT 7
RL23 METJA STANDARD; PRT; 86 AA.
AC P54016;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L23P..
GN RPL23P OR MJ0178.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: TO M.JANASCHII MJ1103.
CC -----
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CC -----
CC EMBL; U67534; AAB98911.1; -.
CC TIGR; MJ0909; -.
CC InterPro; IPR002776; DUF79.
CC Pfam; PF01919; DUF79; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 91 AA; 11146 MW; 4E4260B3466CD72 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
DB 29 KLVF 32

RESULT 9
SPC1 YEAST STANDARD; PRT; 94 AA.
ID _SPC1 YEAST
AC P46965;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Microsomal signal peptidase subunit 1 (EC 3.4.-.-).
GN SPC1 OR YJR0108W.
OS Saccharomyces cerevisiae (Baker's yeast).

```

OC Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB320 / ATCC 37323;  
 RX MEDLINE=96279206; PubMed=8663399;  
 RA Fang H., Panzer S., Mullins C., Hartmann E., Green N.;  
 RT "The homologue of mammalian SPC12 is important for efficient signal  
 RT peptidase activity in *Saccharomyces cerevisiae*.";  
 RL J. Biol. Chem. 271:16460-16465(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288C / FY1679;  
 RA de Haan M., Smits P.H.M., Griveall L.A.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PART OF THE SIGNAL PEPTIDASE COMPLEX (SPC), EXACT  
 CC FUNCTION IS NOT KNOWN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE SPC12 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U6257; AAC49366.1; -;  
 DR EMBL; Z49510; CAA89533.1; -;  
 DR EMBL; Z49511; CAA89535.1; -;  
 DR SCD; S0003770; SPC1.  
 KM Hydrolyase; Protease; Microsome; Endoplasmic reticulum; Transmembrane.  
 FT DOMAIN 1 28 CYTOPLASMIC (POTENTIAL).  
 FT TRANSLEM 29 49 POTENTIAL.  
 FT DOMAIN 50 50 LUMENAL (POTENTIAL).  
 FT TRANSLEM 51 71 POTENTIAL.  
 FT DOMAIN 72 94 CYTOPLASMIC (POTENTIAL).  
 FT SCD 94 94  
 SQ SEQUENCE 94 AA; 10819 MW; 814D7C7A49F49D6D CRC64;  
 Query Match 100.0%; Score 19; DB 1; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 11 KLVF 14  
 RESULT 10  
 PSC3 RAT STANDARD; PRT; 95 AA.  
 AC P02780; Q63463;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Prostatic steroid-binding protein C3 chain precursor (Prostatein  
 DE peptide C3).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83082846; PubMed=6294095;  
 RA Parker M.G., White R., Hurst H., Needham M., Tilly R.;  
 RT "Prostatic steroid-binding protein. Isolation and characterization of  
 RT C3 genes.";  
 RL J. Biol. Chem. 258:12-15(1983).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83238526; PubMed=6190812;

RA Viskochil D.H., Perry S.T., Lea O.A., Stafford D.W., Wilson E.M.,  
 RA French F.S.;  
 RT "Isolation of two genomic sequences encoding the Mr = 14,000 subunit  
 RT of rat prostatein.";  
 RL J. Biol. Chem. 258:8661-8666(1983).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92165796; PubMed=1537831;  
 RA Tan J.A., Marschke K.B., Ho K.-C., Perry S.T., Wilson E.M.,  
 RA French F.S.;  
 RT "Response elements of the androgen-regulated C3 gene.";  
 RL J. Biol. Chem. 267:4456-4466(1992).  
 RN [4]  
 RP ERRATUM.  
 RX MEDLINE=92218467; PubMed=1339454;  
 RA Tan J.A., Marschke K.B., Ho K.C., Perry S.T., Wilson E.M.,  
 RA French F.S.;  
 RL J. Biol. Chem. 267:7958-7958(1992).  
 RN [5]  
 RP SEQUENCE OF 19-95.  
 RX MEDLINE=81188769; PubMed=7014218;  
 RA Peeters B., Rombaerts W., Mous J., Heyns W.;  
 RT "Structural studies on rat prostatic binding protein. The primary  
 RT structure of its glycosylated component C3.";  
 RL Eur. J. Biochem. 115:115-121(1981).  
 CC -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY  
 CC GLYCOPROTEIN OF VENTRAL PROSTATE GLAND. STEROID-BINDING PROTEIN;  
 CC CAN BIND NON-POLAR STEROIDS, CHOLESTEROL AND A GROUP OF SMALL  
 CC PROLINE-RICH PEPTIDES.  
 CC -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED  
 CC C1, C2 AND C3. THESE FORM COVALENT C1:C3 (P) AND C2:C3 (S)  
 CC HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC  
 CC (C1:C3/C3:C2) PROSTATEIN MOLECULES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: VENTRAL PROSTATE.  
 CC -1- INDUCTION: ANDROGEN DEPENDENT, AS SHOWN BY THE DECREASE IN THE  
 CC LEVEL OF THE PROTEIN FOLLOWING CASTRATION.  
 CC -1- MISCELLANEOUS: C3 IS ENCODED BY TWO DIFFERENT GENES.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; V01263; CAA24577.1; -;  
 DR EMBL; M71245; AAA41965.1; -;  
 DR PIR; A03250; BORT3.  
 DR InterPro; IPR003627; Mamgb/prostatn.  
 DR InterPro; IPR000329; Uteroglobln.  
 DR Pfam; PF01099; Uteroglobln; 1.  
 DR Prodom; PD029354; Mamgb/prostatn; 1.  
 DR PROSITE; PS00403; UTEROGLOBIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00404; UTEROGLOBIN\_2; 1.  
 KW Signal; Glycoprotein; Steroid-binding.  
 FT SIGNAL 1 18  
 FT CHAIN 19 95 PROSTATIC STEROID-BINDING PROTEIN C3  
 FT CHAIN  
 FT CARBOHYD 35 35 N-LINKED (GLCNAC... ).  
 FT CONFLICT 53 53 D -> A (IN REF. 3).  
 FT CONFLICT 79 79 G -> S (IN REF. 2).  
 SQ SEQUENCE 95 AA; 10730 MW; F7F7F1A0C882E375 CRC64;  
 Query Match 100.0%; Score 19; DB 1; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 11 KLVF 14

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Db      2 KLVF 5

RESULT 11
VNS2_CVBM
ID _VNS2_CVBM      STANDARD;      PRT; 109 AA.
AC P15774;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Nonstructural protein NS2 (Nonstructural 12.7 kDa protein).
OS Bovine coronavirus (strain Nebus), and
OS Bovine coronavirus (strain F15).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11132, 11129;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mebus;
RX MEDLINE=90320120; PubMed=2142556;
RA Abraham S., Kienzie T.E., Lapps W.E., Brian D.A.;
RT "Sequence and expression analysis of potential nonstructural proteins
RT of 4.9, 4.8, 12.7, and 9.5 kDa encoded between the spike and membrane
RT protein genes of the bovine coronavirus.";
RL Virology 177:488-495 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F15;
RX MEDLINE=90206809; PubMed=2320429;
RA Woloszyn N., Boireau P., Laporte J.;
RT "Nucleotide sequence of the bovine enteric coronavirus BECV F15 mRNA
RT 5 and mRNA 6 unique regions.";
RL Nucleic Acids Res. 18:1303-1303(1990).
CC -!- SIMILARITY: 62% TO CORONAVIRUS MHV-JHM NS2.
CC
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CC
CC EMBL; X51347; CAA35740.1; -.
CC DR EMBL; M31054; AAA42913.1; -.
CC DR PIR; S08408; MNIBH2.
CC DR PIR; C46346; C46346.
CC KW Nonstructural protein.
CC SEQUENCE 109 AA; 12806 MW; 08B7CA339A1BD051 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 89 KLVF 92

RESULT 12
VNS2_CVHC
ID _VNS2_CVHC      STANDARD;      PRT; 109 AA.
AC Q04853;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nonstructural protein NS2 (Nonstructural 12.9 kDa protein).
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=31631;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mebus;
RX MEDLINE=90320120; PubMed=2142556;
RA Abraham S., Kienzie T.E., Lapps W.E., Brian D.A.;
RT "Sequence and expression analysis of potential nonstructural proteins
RT of 4.9, 4.8, 12.7, and 9.5 kDa encoded between the spike and membrane
RT protein genes of the bovine coronavirus.";
RL Virology 177:488-495 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F15;
RX MEDLINE=90206809; PubMed=2320429;
RA Woloszyn N., Boireau P., Laporte J.;
RT "Nucleotide sequence of the bovine enteric coronavirus BECV F15 mRNA
RT 5 and mRNA 6 unique regions.";
RL Nucleic Acids Res. 18:1303-1303(1990).
CC -!- SIMILARITY: 62% TO CORONAVIRUS MHV-JHM NS2.
CC
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CC
CC EMBL; X51347; CAA35740.1; -.
CC DR EMBL; M31054; AAA42913.1; -.
CC DR PIR; S08408; MNIBH2.
CC DR PIR; C46346; C46346.
CC KW Nonstructural protein.
CC SEQUENCE 109 AA; 12806 MW; 08B7CA339A1BD051 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 89 KLVF 92

RESULT 13
YCX1_CHLPY
ID _YCX1_CHLPY      STANDARD;      PRT; 110 AA.
AC P05720;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 12.7 kDa protein in 16S-23S DNA spacer.
OS Chlorella pyrenoidosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86232622; PubMed=3714498;
RA Yamada T., Shimaji M.;
RT "Peculiar feature of the organization of rRNA genes of the Chlorella
RT chloroplast DNA.";
RL Nucleic Acids Res. 14:3827-3839(1986).
CC
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CC
CC EMBL; X03848; CAA27477.1; -.
CC DR EMBL; A24444; A24444.
CC DR PIR; A24444; A24444.
CC KW Chloroplast; Hypothetical protein.
CC SEQUENCE 110 AA; 12782 MW; 1F58A66055A1A377 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 25 KLVF 28

RESULT 14
FOLB_HAEIN

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RX MEDLINE=93297129; PubMed=8517026;
RA Mounir S., Talbot P.J.;
RT "Human coronavirus OC43 RNA 4 lacks two open reading frames located
RT downstream of the S gene of bovine coronavirus.";
RL Virology 192:355-360(1993).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M99576; AAA02569.1; -.
CC DR PIR; A44275; A44275.
CC KW Nonstructural protein.
CC SEQUENCE 109 AA; 12935 MW; 8F06A6E9E30B1667 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 89 KLVF 92

RESULT 13
YCX1_CHLPY
ID _YCX1_CHLPY      STANDARD;      PRT; 110 AA.
AC P05720;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 12.7 kDa protein in 16S-23S DNA spacer.
OS Chlorella pyrenoidosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86232622; PubMed=3714498;
RA Yamada T., Shimaji M.;
RT "Peculiar feature of the organization of rRNA genes of the Chlorella
RT chloroplast DNA.";
RL Nucleic Acids Res. 14:3827-3839(1986).
CC
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CC
CC EMBL; X03848; CAA27477.1; -.
CC DR EMBL; A24444; A24444.
CC DR PIR; A24444; A24444.
CC KW Chloroplast; Hypothetical protein.
CC SEQUENCE 110 AA; 12782 MW; 1F58A66055A1A377 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 25 KLVF 28

RESULT 14
FOLB_HAEIN

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ID  FOLB_HAEIN  STANDARD;  PRT;  118 AA.
AC  P46362;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Dihydropyrimidin aldolase (EC 4.1.2.25) (DHNA).
GN  FOLB OR H10265.
OS  Haemophilus influenzae.
OC  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC  Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=RD / KW20 / ATCC 51907;
RX  MEDLINE=95350630; PubMed=7542800;
RA  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA  Kiehlmann A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA  McKenney K., Sutton G., Fitzhugh W., Fields C.A., Goeyne J.D.,
RA  Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA  Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA  Utechtack T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA  Fane L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA  Grehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA  Venter J.C.;
RT  "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT  R."
RL  Science 269:496-512(1995).
CC  -1- FUNCTION: CATALYZES THE CONVERSION OF 7,8-DIHYDRONEOPTERIN TO 6-
CC  HYDROXYMETHYL-7,8-DIHYDROPTERIN (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: 2-amino-4-hydroxy-6-(D-erythro-1,2,3-
CC  trihydroxypropyl)-7,8-dihydropteridine = 2-amino-4-hydroxy-6-
CC  hydroxymethyl-7,8-dihydropteridine + glycolaldemhyde.
CC  -1- PATHWAY: Folate biosynthesis.
CC  -1- SIMILARITY: BELONGS TO THE DHNA FAMILY.
-----
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-----
CC  EMBL; U32712; AAC21930.1; -.
CC  TIGR; H10265; -.
DR  InterPro; IPR003098; FOLB.
DR  Pfam; PF02152; FOLB; 1.
DR  TIGRPFAM; TIGR00525; FOLB; 1.
DR  TIGRPFAM; TIGR00526; FOLB_dom; 1.
KW  Lyase; Folate biosynthesis; Complete proteome.
SQ  SEQUENCE 118 AA; 13577 MW; 158C716C473DC701 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
    |||
    |||
Db 27 KLVF 30

RESULT 15
R22B YEAST
ID R22B YEAST STANDARD; PRT; 121 AA.
AC P56626;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S ribosomal protein L22-B.
GN RPL22B OR YFL034BC.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.

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OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasamura S.-I., Sasamura M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RL Nat. Genet. 10:261-268(1995).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L22 IN YEAST.
CC -1- SIMILARITY: BELONGS TO THE L22B FAMILY OF RIBOSOMAL PROTEINS.
-----
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-----
CC EMBL; D50617; -; NOT_ANNOTATED_CDS.
CC SGD; S0006436; RPL22B.
DR InterPro; IPR002671; Ribosomal L22e.
DR Pfam; PF01776; Ribosomal L22e; 1.
DR ProDom; PD007306; Ribosomal L22e; 1.
KW Ribosomal protein, Multigene family.
FT INIT MET 0
SQ SEQUENCE 121 AA; 13695 MW; 2A0A3EF175C20A26 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
    |||
    |||
Db 103 KLVF 106

Search completed: January 3, 2003, 07:43:17
Job time : 13 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:42:56 ; Search time 29 Seconds  
(without alignments)  
28.420 Million cell updates/sec

Title: US-09-867-847-15  
Perfect score: 19  
Sequence: 1 KLVF 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_prodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_rvirus:\*  
17: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	14	4	Q9UH91
2	19	100.0	19	4	Q9UC8
3	19	100.0	27	1	Q9UW8
4	19	100.0	28	4	Q9UCD1
5	19	100.0	30	4	Q9UCA9
6	19	100.0	33	4	Q9UC33
7	19	100.0	47	1	Q52455
8	19	100.0	48	5	Q9GR26
9	19	100.0	51	12	Q8QMN2
10	19	100.0	52	8	Q9MEH0
11	19	100.0	54	16	Q8RBV2
12	19	100.0	57	16	Q92IT0
13	19	100.0	58	12	Q39633
14	19	100.0	61	2	Q9AFZ0
15	19	100.0	62	9	Q8W6C9
16	19	100.0	63	6	Q8SPJ7

17	19	100.0	64	5	Q9NH7	Q9nh7 drosophila
18	19	100.0	65	5	Q94144	Q94144 caenorhabdi
19	19	100.0	67	16	Q92IF4	Q92if4 rickettsia
20	19	100.0	69	10	Q9SMP2	Q9smp2 arabidopsis
21	19	100.0	71	16	Q8UC16	Q8uc16 agrobacteri
22	19	100.0	72	5	Q25925	Q25925 plasmodium
23	19	100.0	74	2	Q936G7	Q936g7 staphylococ
24	19	100.0	76	2	Q8VVM4	Q8vvm4 escherichia
25	19	100.0	76	8	Q9TBS6	Q9tbs6 toxostoma 1
26	19	100.0	76	8	Q9TBS2	Q9tbs2 toxostoma r
27	19	100.0	77	2	Q54879	Q54879 streptococ
28	19	100.0	78	17	Q9HPR1	Q9hpr1 halobacteri
29	19	100.0	79	4	Q969F3	Q969f3 homo sapien
30	19	100.0	79	11	Q35463	Q35463 cricetus
31	19	100.0	79	16	Q92GT7	Q92gt7 rickettsia
32	19	100.0	81	5	Q96183	Q96183 plasmodium
33	19	100.0	82	4	Q16014	Q16014 homo sapien
34	19	100.0	82	4	Q16019	Q16019 homo sapien
35	19	100.0	82	4	Q16020	Q16020 homo sapien
36	19	100.0	82	4	P78438	P78438 homo sapien
37	19	100.0	83	16	Q8UC93	Q8uc93 agrobacteri
38	19	100.0	84	16	Q8YH11	Q8yh11 bruceella me
39	19	100.0	85	8	Q9TBS4	Q9tbs4 toxostoma g
40	19	100.0	85	8	Q9TBS0	Q9tbs0 toxostoma c
41	19	100.0	85	8	Q9TBR8	Q9tbr8 toxostoma c
42	19	100.0	85	8	Q9TBR6	Q9tbr6 toxostoma c
43	19	100.0	85	8	Q9TBR4	Q9tbr4 oreoscoptes
44	19	100.0	85	8	Q9TBR2	Q9tbr2 toxostoma b
45	19	100.0	85	8	Q9TBR0	Q9tbr0 toxostoma c

ALIGNMENTS

RESULT 1

Q9UH91 PRELIMINARY; PRT; 14 AA.  
AC Q9UH91;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Xanthine oxidoreductase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20487118; Pubmed=11034305;  
RA Martelin E., Palvimo J.J., Lapatto R., Raitvio K.O.;  
RT "Nuclear factor Y activates the human xanthine oxidoreductase gene  
RT promoter";  
RL FEBS Lett. 480:84-88(2000).  
DR EMBL; AF203979; AAF15890.1; -.  
FT NON TER 14  
SQ SEQUENCE 14 AA; 1626 MW; D300F701792F0D2 CRC64;

Query Match Score 19; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 5 KLVF 8  
RESULT 2  
Q9UC8 PRELIMINARY; PRT; 19 AA.  
ID Q9UC8;  
AC Q9UC8;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE Beta-amyloid-(1-42) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94068497; PubMed=8248178;  
RA Rohrer A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,  
RA Gowing E., Ball M.J.;  
RT "Beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid  
RT deposits; implications for the pathology of Alzheimer disease.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).  
DR HSSP; P05067; IAMB.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
SQ SEQUENCE 19 AA; 2315 MW; 05B02B3F6DCE3E CRC64;  
  
Query Match 100.0%; Score 19; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVP 4  
Db 16 KLVP 19  
  
RESULT 3  
Q9UWG8 PRELIMINARY; PRT; 27 AA.  
AC Q9UWG8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Keto-valine-ferredoxin oxidoreductase delta-subunit, VOR delta  
DE (Fragment).  
OS Thermococcus sp. (strain KI).  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=35749;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=ES-1;  
RX MEDLINE=96146528; PubMed=8550513;  
RA Heider J., Mai X., Adams M.W.;  
RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a  
RT new and reversible coenzyme A-dependent enzyme involved in peptide  
RT fermentation by hyperthermophilic archaea.";  
RL J. Bacteriol. 178:780-787(1996).  
SQ SEQUENCE 27 AA; 3046 MW; 60C56F313C76B16C CRC64;  
  
Query Match 100.0%; Score 19; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVP 4  
Db 14 KLVP 17  
  
RESULT 4  
Q9UCD1 PRELIMINARY; PRT; 28 AA.  
AC Q9UCD1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Beta-amyloid peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=94045585; PubMed=8229004;  
RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;  
RT "Characterization of beta-amyloid peptide from human cerebrospinal  
RT fluid.";  
RL J. Neurochem. 61:1965-1968(1993).  
DR HSSP; P05067; IAMB.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;  
  
Query Match 100.0%; Score 19; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVP 4  
Db 16 KLVP 19  
  
RESULT 5  
Q9UCA9 PRELIMINARY; PRT; 30 AA.  
AC Q9UCA9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Beta-amyloid protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94153015; PubMed=8109908;  
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;  
RT "The amino acid sequence of neuritic plaque amyloid from a familial  
RT Alzheimer's disease patient.";  
RL Ann. Neurol. 35:245-246(1994).  
DR HSSP; P05067; IBA4.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;  
  
Query Match 100.0%; Score 19; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVP 4  
Db 16 KLVP 19  
  
RESULT 6  
Q9UC33 PRELIMINARY; PRT; 33 AA.  
AC Q9UC33;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Beta-amyloid peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93024877; PubMed=1406936;  
RA Seubert P., Vigo-Pelfrey C., Esch P., Lee M., Dovey H., Davis D.,  
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;  
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from  
RT biological fluids.";  
RL Nature 359:325-327(1992).



DR HSSP: P05067; 1BA4.  
 DR InterPro: IPR001255; Beta-APP.  
 DR Pfam: PF03494; Beta-APP; 1.  
 SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 100.0%; Score 19; DB 4; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 16 KLVF 19

RESULT 7  
 ID Q52455 PRELIMINARY; PRT; 47 AA.  
 AC Q52455;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-JUN-1998 (TEMBLrel. 06, Last annotation update)  
 DE Orf A (Fragment).  
 OS Pyrococcus sp.  
 OC Archaea: Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 NC NCB1\_TaxID=33866;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IFREMER 585;  
 RX MEDLINE=96144265; PubMed=8566767;  
 RA Bouyoub A., Barbier G., Querellou J., Forterre P.;  
 RT "A putative SOS repair gene (dinf-like) in a hyperthermophilic  
 archaeon.";  
 RL Gene 167:147-149 (1995).  
 DR EMBL: X91006; CAA62486.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 47 AA; 5541 MW; 828FC50C94800802 CRC64;

Query Match 100.0%; Score 19; DB 1; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 6 KLVF 9

RESULT 8  
 ID Q9GR26 PRELIMINARY; PRT; 48 AA.  
 AC Q9GR26;  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
 DE Elongation factor-lalpha (Fragment).  
 GN EF-1ALPHA.  
 OS Aphidius colemani (Aphid parasite).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
 OC Ichneumonidae; Braconidae; Aphidinae; Aphidius.  
 NC NCB1\_TaxID=78482;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sanchez A., Beishaw R., Michelena J., Latorre A., Quicke D.,  
 RA Gardenfors U.;  
 RT "The phylogenetic analysis of variable length sequence data: elongation  
 factor-lalpha intons in European populations of the parasitoid wasp  
 RT Paeusia (Hymenoptera: Braconidae: Aphidinae).";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ01978; CAC19825.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 48 AA; 5593 MW; 5FF20AA7979B6D16 CRC64;

Query Match 100.0%; Score 19; DB 5; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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 DB 32 KLVF 35

RESULT 9  
 ID Q8QMN2 PRELIMINARY; PRT; 51 AA.  
 AC Q8QMN2;  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
 DE V206.  
 OS Cowpox virus (CPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NC NCB1\_TaxID=10243;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=83117629; PubMed=6961398;  
 RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;  
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of  
 RT repeated and unique sequence elements.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116 (1982).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=90177240; PubMed=2309453;  
 RA Parsons B.L., Pickup D.J.;  
 RT "Transcription of orthopoxvirus telomeres at late times during  
 RT infection.";  
 RL Virology 175:69-80 (1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=91196263; PubMed=2014645;  
 RA Hu F.Q., Pickup D.J.;  
 RT "Transcription of the terminal loop region of vaccinia virus DNA is  
 RT initiated from the telomere sequences directing DNA resolution.";  
 RL Virology 181:716-720 (1991).

RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=94378510; PubMed=8091665;  
 RA Hu F.Q., Smith C.A., Pickup D.J.;  
 RT "Cowpox virus contains two copies of an early gene encoding a soluble  
 RT secreted form of the type II TNF receptor.";  
 RL Virology 204:343-356 (1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RA Pickup D.J.;  
 RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.

RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF482758; AAM13654.1; -.  
 SQ SEQUENCE 51 AA; 6002 MW; 97429938CAB1D4B5 CRC64;

Query Match 100.0%; Score 19; DB 12; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 16 KLVF 19

RESULT 10
ID Q9MEHO PRELIMINARY; PRT; 52 AA.
AC Q9MEHO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Megacytiophanes norvegica.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Euphausiacea; Euphausiidae; Megacytiophanes.
OX NCBI_TaxID=48144;
RN [1]
RP SEQUENCE FROM N.A.
RA Zane L., Ostellari L., Maccatrozzo L., Bargelloni L., Cuzin-Roudy J.,
RA Buchholz F., Patarnello T.;
RA "Genetic differentiation in a pelagic crustacean (Megacytiophanes
RT norvegica, Euphausiacea) from the North East Atlantic and the
RT Mediterranean Sea.";
RT Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RL
DR EMBL; AF150623; AAF73171.1; -
DR EMBL; AF150612; AAF73160.1; -
DR EMBL; AF150613; AAF73161.1; -
DR EMBL; AF150614; AAF73162.1; -
DR EMBL; AF150615; AAF73163.1; -
DR EMBL; AF150616; AAF73164.1; -
DR EMBL; AF150617; AAF73165.1; -
DR EMBL; AF150618; AAF73166.1; -
DR EMBL; AF150619; AAF73167.1; -
DR EMBL; AF150620; AAF73168.1; -
DR EMBL; AF150621; AAF73169.1; -
DR EMBL; AF150622; AAF73170.1; -
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 6120 MW; 041571A67AF9D16D CRC64;

Query Match 100.0%; Score 19; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 27 KLVF 30

RESULT 11
Q9RBV2 PRELIMINARY; PRT; 54 AA.
AC Q9RBV2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE0706.
GN TTE0706.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;

RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AB013039; AAM23968.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 54 AA; 6436 MW; 7EA021E52840EC15 CRC64;

Query Match 100.0%; Score 19; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 7 KLVF 10

RESULT 12
Q92ITO PRELIMINARY; PRT; 57 AA.
AC Q92ITO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein RC0340.
GN RC0340.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008599; AAL02878.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 57 AA; 6509 MW; 43A414C10AE77085 CRC64;

Query Match 100.0%; Score 19; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 52 KLVF 55

RESULT 13
O39633 PRELIMINARY; PRT; 58 AA.
AC O39633;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae.
OX NCBI_TaxID=11975;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LYMINGTON/94/UK;
RX MEDLINE=97278118; PubMed=9131452;
RA Green S.M., Lambden P.R., Owen Caul E., Clarke I.N.;
RT "Capsid sequence diversity in small round structured viruses from
RL J. Med. Virol. 52:14-19(1997).
DR EMBL; Z73995; CAA98301.1; -.
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
FT NON_TER 1
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FT NON\_TER 58 58  
SQ SEQUENCE 58 AA; 6159 MW; A2D51FD32B3B5E81 CRC64;

Query Match 100.0%; Score 19; DB 12; Length 58;

Best Local Similarity 100.0%; Pred. No. 4.5e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVF 4  
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Db 18 KLVF 21

Db 19 KLVF 22

Search completed: January 3, 2003, 07:44:37  
Job time : 31 secs

## RESULT 14

O9AFZ0 PRELIMINARY; PRT; 61 AA.  
AC O9AFZ0;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 1S91 orfA.  
GN S0020.  
OS Shigella flexneri.  
OC plasmid virulence plasmid pWR501.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Shigella.  
OX NCBI\_TaxID=623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21189246; PubMed=11292750;  
RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,  
RT Blatner F.R.;  
RT "Complete DNA sequence and analysis of the large virulence plasmid of  
RT Shigella flexneri.";  
RL Infect. Immun. 69:3271-3285(2001).  
DR EMBL: AF348706; AAK18331.1; -.  
KW plasmid.  
SQ SEQUENCE 61 AA; 6864 MW; 49C34FBA7B8DC228 CRC64;

Query Match 100.0%; Score 19; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVF 4  
|||  
Db 7 KLVF 10

## RESULT 15

O8W6C9 PRELIMINARY; PRT; 62 AA.  
AC O8W6C9;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE MemB4.  
GN ORF62.  
OS Vibrio phage VSK.  
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.  
OX NCBI\_TaxID=181604;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Basu N., Kar S., Ghosh R.K.;  
RT "Molecular analysis of filamentous phage VSK of Vibrio cholerae 0139:  
RT A possible clue to genetic transmission.";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF453500; AAL49745.1; -.  
SQ SEQUENCE 62 AA; 7221 MW; 56813397E7BC2BDF CRC64;

Query Match 100.0%; Score 19; DB 9; Length 62;

Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLVF 4



GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: January 3, 2003, 07:52:07 ; Search time 15 Seconds  
(without alignments)  
7.846 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 4

Sequence: 1 KLVF 4

## Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

## Post-processing: Listing first 1000 summaries

## Database :

Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance, to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	4	3	US-08-970-833-1
2	4	100.0	4	3	US-08-664-379B-17
3	4	100.0	4	4	US-09-095-106A-25
4	4	100.0	5	1	US-08-127-904-15
5	4	100.0	5	2	US-08-612-785B-10
6	4	100.0	5	3	US-08-970-833-2
7	4	100.0	5	4	US-08-703-675C-46
8	4	100.0	5	4	US-09-242-724-25
9	4	100.0	5	4	US-09-242-724-26
10	4	100.0	5	4	US-08-617-267C-10
11	4	100.0	5	4	US-09-095-106A-1
12	4	100.0	5	4	US-08-612-785B-9
13	4	100.0	5	4	US-09-095-106A-19
14	4	100.0	5	4	US-09-095-106A-13
15	4	100.0	5	5	PCT-US94-10475-15
16	4	100.0	6	2	US-08-612-785B-9
17	4	100.0	6	2	US-08-612-785B-31
18	4	100.0	6	3	US-08-664-379B-19
19	4	100.0	6	4	US-08-703-675C-31
20	4	100.0	6	4	US-08-703-675C-32
21	4	100.0	6	4	US-08-703-675C-44
22	4	100.0	6	4	US-09-242-724-24
23	4	100.0	6	4	US-09-242-724-27
24	4	100.0	6	4	US-09-242-724-30
25	4	100.0	6	4	US-09-242-724-31
26	4	100.0	6	4	US-09-242-724-31
27	4	100.0	6	4	US-09-242-724-33

28	4	100.0	6	4	US-08-617-267C-8	Sequence 8, Appl
29	4	100.0	6	4	US-08-617-267C-9	Sequence 9, Appl
30	4	100.0	6	4	US-08-617-267C-31	Sequence 31, Appl
31	4	100.0	6	4	US-08-617-267C-43	Sequence 43, Appl
32	4	100.0	6	4	US-09-095-106A-5	Sequence 5, Appl
33	4	100.0	6	4	US-09-095-106A-15	Sequence 15, Appl
34	4	100.0	7	1	US-08-127-904-14	Sequence 14, Appl
35	4	100.0	7	2	US-08-612-785B-6	Sequence 6, Appl
36	4	100.0	7	2	US-08-612-785B-7	Sequence 7, Appl
37	4	100.0	7	4	US-08-703-675C-29	Sequence 29, Appl
38	4	100.0	7	4	US-08-703-675C-30	Sequence 30, Appl
39	4	100.0	7	4	US-08-617-267C-6	Sequence 6, Appl
40	4	100.0	7	4	US-08-617-267C-7	Sequence 7, Appl
41	4	100.0	7	4	US-09-264-709A-13	Sequence 13, Appl
42	4	100.0	7	4	US-09-095-106A-11	Sequence 11, Appl
43	4	100.0	7	4	US-09-095-106A-12	Sequence 12, Appl
44	4	100.0	7	5	PCT-US94-10475-14	Sequence 14, Appl
45	4	100.0	8	1	US-08-457-804-1	Sequence 1, Appl
46	4	100.0	8	1	US-08-457-804-6	Sequence 6, Appl
47	4	100.0	8	1	US-08-457-804-7	Sequence 7, Appl
48	4	100.0	8	2	US-08-612-785B-5	Sequence 5, Appl
49	4	100.0	8	2	US-08-630-645-1	Sequence 1, Appl
50	4	100.0	8	4	US-08-703-675C-28	Sequence 28, Appl
51	4	100.0	8	4	US-08-617-267C-5	Sequence 5, Appl
52	4	100.0	8	4	US-09-095-106A-8	Sequence 8, Appl
53	4	100.0	8	4	US-09-095-106A-9	Sequence 9, Appl
54	4	100.0	8	4	US-09-095-106A-44	Sequence 44, Appl
55	4	100.0	8	4	US-08-766-596A-1	Sequence 1, Appl
56	4	100.0	8	5	PCT-US96-10220-1	Sequence 1, Appl
57	4	100.0	9	4	US-09-264-709A-4	Sequence 4, Appl
58	4	100.0	9	4	US-09-095-106A-7	Sequence 7, Appl
59	4	100.0	9	4	US-09-095-106A-6	Sequence 6, Appl
60	4	100.0	9	4	US-08-766-596A-53	Sequence 53, Appl
61	4	100.0	9	4	US-08-766-596A-54	Sequence 54, Appl
62	4	100.0	9	4	US-08-766-596A-64	Sequence 64, Appl
63	4	100.0	10	3	US-08-970-833-3	Sequence 3, Appl
64	4	100.0	10	4	US-09-095-106A-2	Sequence 2, Appl
65	4	100.0	11	2	US-08-630-645-14	Sequence 14, Appl
66	4	100.0	11	3	US-08-970-833-8	Sequence 8, Appl
67	4	100.0	11	4	US-08-766-596A-14	Sequence 14, Appl
68	4	100.0	11	4	US-08-766-596A-68	Sequence 68, Appl
69	4	100.0	11	5	PCT-US96-10220-14	Sequence 14, Appl
70	4	100.0	15	2	US-08-480-190-39	Sequence 39, Appl
71	4	100.0	15	2	US-08-612-785B-4	Sequence 4, Appl
72	4	100.0	15	2	US-08-612-785B-14	Sequence 14, Appl
73	4	100.0	15	2	US-08-612-785B-37	Sequence 37, Appl
74	4	100.0	15	2	US-08-488-379-39	Sequence 39, Appl
75	4	100.0	15	4	US-08-617-267C-14	Sequence 14, Appl
76	4	100.0	15	4	US-08-617-267C-14	Sequence 14, Appl
77	4	100.0	15	4	US-08-766-596A-56	Sequence 56, Appl
78	4	100.0	15	4	US-08-766-596A-57	Sequence 57, Appl
79	4	100.0	15	4	US-08-766-596A-58	Sequence 58, Appl
80	4	100.0	15	4	US-08-766-596A-60	Sequence 60, Appl
81	4	100.0	15	4	US-08-766-596A-61	Sequence 61, Appl
82	4	100.0	15	4	US-08-766-596A-63	Sequence 63, Appl
83	4	100.0	15	4	US-08-766-596A-65	Sequence 65, Appl
84	4	100.0	15	5	PCT-US93-07545-39	Sequence 39, Appl
85	4	100.0	17	4	US-09-264-709A-2	Sequence 2, Appl
86	4	100.0	19	3	US-08-970-833-11	Sequence 11, Appl
87	4	100.0	20	3	US-08-970-833-10	Sequence 10, Appl
88	4	100.0	23	2	US-08-505-486-75	Sequence 75, Appl
89	4	100.0	23	3	US-08-801-028-75	Sequence 75, Appl
90	4	100.0	23	3	US-09-340-154-75	Sequence 75, Appl
91	4	100.0	23	3	US-09-482-611B-75	Sequence 75, Appl
92	4	100.0	23	5	PCT-US95-09338-75	Sequence 75, Appl
93	4	100.0	23	5	PCT-US95-09338-75	Sequence 75, Appl
94	4	100.0	26	1	US-08-304-585-7	Sequence 7, Appl
95	4	100.0	27	1	US-08-141-324-11	Sequence 11, Appl
96	4	100.0	27	1	US-08-141-324-12	Sequence 12, Appl
97	4	100.0	27	1	US-08-541-902-11	Sequence 11, Appl
98	4	100.0	27	1	US-08-541-902-12	Sequence 12, Appl
99	4	100.0	27	2	US-08-505-486-76	Sequence 76, Appl
100	4	100.0	27	2	US-08-505-486-77	Sequence 77, Appl

101	4	100.0	27	3	US-08-801-028-76	Sequence 76, Appl	174	4	100.0	40	5	PCT-US92-06700-1	Sequence 1, Appli
102	4	100.0	27	3	US-08-801-028-77	Sequence 77, Appl	175	4	100.0	41	1	US-07-819-361-1	Sequence 1, Appli
103	4	100.0	27	3	US-08-963-121C-9	Sequence 9, Appli	176	4	100.0	41	1	US-08-302-808-4	Sequence 4, Appli
104	4	100.0	27	3	US-09-340-154-76	Sequence 76, Appl	177	4	100.0	41	2	US-08-682-245A-3	Sequence 3, Appli
105	4	100.0	27	3	US-09-340-154-77	Sequence 77, Appl	178	4	100.0	41	2	US-08-986-948-4	Sequence 4, Appli
106	4	100.0	27	4	US-09-543-153-9	Sequence 9, Appli	179	4	100.0	42	1	US-07-744-767A-2	Sequence 2, Appli
107	4	100.0	27	4	US-09-482-611B-76	Sequence 76, Appl	180	4	100.0	42	1	US-08-179-574-1	Sequence 1, Appli
108	4	100.0	27	4	US-09-482-611B-77	Sequence 77, Appl	181	4	100.0	42	1	US-08-271-162-5	Sequence 5, Appli
109	4	100.0	27	5	PCT-US95-04803-10	Sequence 10, Appl	182	4	100.0	42	1	US-08-347-144-1	Sequence 1, Appli
110	4	100.0	27	5	PCT-US95-09338-76	Sequence 76, Appl	183	4	100.0	42	1	US-08-462-859A-19	Sequence 19, Appl
111	4	100.0	27	5	PCT-US95-09338-77	Sequence 77, Appl	184	4	100.0	42	1	US-08-123-659A-19	Sequence 19, Appl
112	4	100.0	27	5	PCT-US95-09339-76	Sequence 76, Appl	185	4	100.0	42	1	US-08-464-247A-19	Sequence 19, Appl
113	4	100.0	27	5	PCT-US95-09339-77	Sequence 77, Appl	186	4	100.0	42	1	US-08-464-248A-19	Sequence 19, Appl
114	4	100.0	28	1	US-08-346-849-4	Sequence 4, Appli	187	4	100.0	42	1	US-08-476-464A-1	Sequence 1, Appli
115	4	100.0	28	1	US-08-302-808-7	Sequence 7, Appli	188	4	100.0	42	1	US-08-304-585-2	Sequence 2, Appli
116	4	100.0	28	2	US-08-609-090-2	Sequence 2, Appli	189	4	100.0	42	1	US-08-302-808-5	Sequence 5, Appli
117	4	100.0	28	2	US-08-986-948-7	Sequence 7, Appli	190	4	100.0	42	1	US-08-268-348A-1	Sequence 1, Appli
118	4	100.0	28	2	US-08-233-284A-4	Sequence 4, Appli	191	4	100.0	42	1	US-08-268-348A-2	Sequence 2, Appli
119	4	100.0	28	2	US-08-461-216-2	Sequence 2, Appli	192	4	100.0	42	1	US-08-268-348A-3	Sequence 3, Appli
120	4	100.0	28	4	US-09-388-890-2	Sequence 2, Appli	193	4	100.0	42	1	US-08-268-348A-4	Sequence 4, Appli
121	4	100.0	28	4	US-09-388-890-3	Sequence 3, Appli	194	4	100.0	42	1	US-08-268-348A-5	Sequence 5, Appli
122	4	100.0	28	4	US-09-388-890-4	Sequence 4, Appli	195	4	100.0	42	1	US-08-268-348A-6	Sequence 6, Appli
123	4	100.0	28	4	US-09-388-890-5	Sequence 5, Appli	196	4	100.0	42	2	US-08-433-734-2	Sequence 2, Appli
124	4	100.0	28	4	US-09-388-890-6	Sequence 6, Appli	197	4	100.0	42	2	US-08-609-090-9	Sequence 9, Appli
125	4	100.0	28	4	US-09-388-890-7	Sequence 7, Appli	198	4	100.0	42	2	US-07-737-371E-72	Sequence 72, Appl
126	4	100.0	28	4	US-09-388-890-8	Sequence 8, Appli	199	4	100.0	42	2	US-08-422-333-4	Sequence 4, Appli
127	4	100.0	28	4	US-09-388-890-9	Sequence 9, Appli	200	4	100.0	42	2	US-08-682-245A-4	Sequence 4, Appli
128	4	100.0	28	4	US-09-388-890-10	Sequence 10, Appl	201	4	100.0	42	2	US-08-986-948-5	Sequence 5, Appli
129	4	100.0	28	4	US-09-388-890-12	Sequence 12, Appl	202	4	100.0	42	3	US-08-717-551A-2	Sequence 2, Appli
130	4	100.0	28	4	US-09-388-890-13	Sequence 13, Appl	203	4	100.0	42	4	US-09-388-890-1	Sequence 1, Appli
131	4	100.0	28	4	US-09-388-890-14	Sequence 14, Appl	204	4	100.0	42	4	US-09-005-215-20	Sequence 20, Appl
132	4	100.0	28	4	US-09-264-709A-1	Sequence 1, Appli	205	4	100.0	42	4	US-09-242-724-23	Sequence 23, Appl
133	4	100.0	28	4	US-08-723-661B-2	Sequence 2, Appli	206	4	100.0	42	4	US-08-922-930-2	Sequence 2, Appli
134	4	100.0	30	2	US-08-609-090-3	Sequence 3, Appli	207	4	100.0	42	5	PCT-US92-06700-2	Sequence 2, Appli
135	4	100.0	33	2	US-08-609-090-4	Sequence 4, Appli	208	4	100.0	42	5	PCT-US93-00325-1	Sequence 1, Appli
136	4	100.0	34	2	US-08-475-579A-4	Sequence 4, Appli	209	4	100.0	42	5	PCT-US95-08302-5	Sequence 5, Appli
137	4	100.0	35	1	US-08-304-585-6	Sequence 6, Appli	210	4	100.0	42	6	5220013-12	Patent No. 5220013
138	4	100.0	35	2	US-08-612-785B-15	Sequence 15, Appl	211	4	100.0	42	6	5223482-12	Patent No. 5223482
139	4	100.0	35	2	US-08-612-785B-16	Sequence 16, Appl	212	4	100.0	43	1	US-08-235-400-1	Sequence 1, Appli
140	4	100.0	35	2	US-08-612-785B-36	Sequence 36, Appl	213	4	100.0	43	1	US-08-437-067-1	Sequence 1, Appli
141	4	100.0	35	2	US-08-612-785B-38	Sequence 38, Appl	214	4	100.0	43	1	US-08-302-808-6	Sequence 6, Appli
142	4	100.0	35	2	US-08-612-785B-40	Sequence 40, Appl	215	4	100.0	43	1	US-08-079-511-1	Sequence 1, Appli
143	4	100.0	35	4	US-08-617-267C-15	Sequence 15, Appl	216	4	100.0	43	1	US-08-467-607-1	Sequence 1, Appli
144	4	100.0	35	4	US-08-617-267C-16	Sequence 16, Appl	217	4	100.0	43	1	US-08-404-831-1	Sequence 1, Appli
145	4	100.0	35	4	US-09-149-476-711	Sequence 711, App	218	4	100.0	43	2	US-08-602-264A-3	Sequence 3, Appli
146	4	100.0	36	2	US-08-609-090-6	Sequence 6, Appli	219	4	100.0	43	2	US-08-469-363-1	Sequence 1, Appli
147	4	100.0	37	4	US-09-330-914A-10	Sequence 10, Appl	220	4	100.0	43	2	US-08-612-785B-1	Sequence 1, Appli
148	4	100.0	38	1	US-08-302-808-1	Sequence 1, Appli	221	4	100.0	43	2	US-08-475-579A-1	Sequence 1, Appli
149	4	100.0	38	2	US-07-737-371E-68	Sequence 68, Appl	222	4	100.0	43	2	US-08-850-392-1	Sequence 1, Appli
150	4	100.0	38	2	US-08-986-948-1	Sequence 1, Appli	223	4	100.0	43	2	US-07-737-371E-70	Sequence 70, Appl
151	4	100.0	38	4	US-09-149-476-491	Sequence 491, App	224	4	100.0	43	2	US-08-986-948-6	Sequence 6, Appli
152	4	100.0	38	6	5262332-1	Patent No. 5262332	225	4	100.0	43	2	US-08-975-977-1	Sequence 1, Appli
153	4	100.0	39	1	US-08-304-585-5	Sequence 5, Appli	226	4	100.0	43	2	US-08-817-423-1	Sequence 1, Appli
154	4	100.0	39	1	US-08-302-808-2	Sequence 2, Appli	227	4	100.0	43	2	US-08-920-162A-1	Sequence 1, Appli
155	4	100.0	39	2	US-08-609-090-7	Sequence 7, Appli	228	4	100.0	43	3	US-08-461-018A-3	Sequence 3, Appli
156	4	100.0	39	2	US-08-682-245A-1	Sequence 1, Appli	229	4	100.0	43	3	US-08-976-191-1	Sequence 1, Appli
157	4	100.0	39	2	US-08-986-948-2	Sequence 2, Appli	230	4	100.0	43	3	US-08-339-141A-1	Sequence 1, Appli
158	4	100.0	40	1	US-07-744-767A-1	Sequence 1, Appli	231	4	100.0	43	3	US-08-976-179-1	Sequence 1, Appli
159	4	100.0	40	1	US-08-235-400-2	Sequence 2, Appli	232	4	100.0	43	4	US-09-216-958-3	Sequence 3, Appli
160	4	100.0	40	1	US-08-476-464A-2	Sequence 2, Appli	233	4	100.0	43	4	US-09-356-931-1	Sequence 1, Appli
161	4	100.0	40	1	US-08-304-585-1	Sequence 1, Appli	234	4	100.0	43	4	US-08-733-202-1	Sequence 1, Appli
162	4	100.0	40	1	US-08-304-585-8	Sequence 8, Appli	235	4	100.0	43	4	US-08-703-675C-1	Sequence 1, Appli
163	4	100.0	40	1	US-08-302-808-3	Sequence 3, Appli	236	4	100.0	43	4	US-09-390-693-1	Sequence 1, Appli
164	4	100.0	40	2	US-08-433-734-1	Sequence 1, Appli	237	4	100.0	43	4	US-08-617-267C-1	Sequence 1, Appli
165	4	100.0	40	2	US-08-609-090-8	Sequence 8, Appli	238	4	100.0	43	4	US-09-303-655-1	Sequence 1, Appli
166	4	100.0	40	2	US-07-737-371E-69	Sequence 69, Appl	239	4	100.0	43	4	US-08-294-819-1	Sequence 1, Appli
167	4	100.0	40	2	US-08-682-245A-2	Sequence 2, Appli	240	4	100.0	43	5	PCT-US95-14659-1	Patent No. 5187153
168	4	100.0	40	2	US-08-986-948-3	Sequence 3, Appli	241	4	100.0	43	6	5223482-14	Patent No. 5223482
169	4	100.0	40	2	US-08-461-216-1	Sequence 1, Appli	242	4	100.0	44	6	5223482-14	Patent No. 5187153
170	4	100.0	40	4	US-08-959-148-1	Sequence 1, Appli	243	4	100.0	47	2	US-08-609-090-10	Sequence 10, Appl
171	4	100.0	40	4	US-08-242-724-22	Sequence 22, Appl	244	4	100.0	52	2	US-08-609-090-11	Sequence 11, Appl
172	4	100.0	40	4	US-08-723-661B-1	Sequence 1, Appli	245	4	100.0	53	4	US-09-173-887-5	Sequence 5, Appli
173	4	100.0	40	4	US-09-062-365-3	Sequence 3, Appli	246	4	100.0				

247	4	100.0	53	4	US-09-294-987-1	Sequence 1, Appl1	320	4	100.0	227	4	US-08-801-740-5	Sequence 5, Appl1
248	4	100.0	59	1	US-08-484-869-3	Sequence 3, Appl1	321	4	100.0	230	4	US-09-071-035-372	Sequence 372, App
249	4	100.0	59	1	US-08-472-627-3	Sequence 3, Appl1	322	4	100.0	236	4	US-09-292-412-2	Sequence 2, Appl1
250	4	100.0	59	1	US-08-388-463-3	Sequence 3, Appl1	323	4	100.0	258	1	US-07-990-301A-2	Sequence 2, Appl1
251	4	100.0	60	4	US-09-638-715-21	Sequence 21, Appl1	324	4	100.0	260	4	US-09-134-001C-4009	Sequence 4009, Ap
252	4	100.0	63	1	US-08-462-859A-3	Sequence 3, Appl1	325	4	100.0	264	1	US-07-990-893-5	Sequence 5, Appl1
253	4	100.0	63	1	US-08-462-859A-3	Sequence 3, Appl1	326	4	100.0	266	4	US-08-983-502-20	Sequence 20, Appl
254	4	100.0	63	1	US-08-123-659A-3	Sequence 4, Appl1	327	4	100.0	266	5	PCT-US96-10521-20	Sequence 20, Appl
255	4	100.0	63	1	US-08-123-659A-3	Sequence 4, Appl1	328	4	100.0	270	4	US-08-961-083-64	Sequence 64, Appl
256	4	100.0	63	1	US-08-464-247A-3	Sequence 3, Appl1	329	4	100.0	282	4	US-09-134-001C-3155	Sequence 3155, Ap
257	4	100.0	63	1	US-08-464-247A-3	Sequence 4, Appl1	330	4	100.0	286	4	US-09-360-017-1	Sequence 1, Appl1
258	4	100.0	63	1	US-08-464-248A-3	Sequence 3, Appl1	331	4	100.0	286	4	US-09-134-001C-3059	Sequence 3059, Ap
259	4	100.0	63	1	US-08-464-248A-4	Sequence 4, Appl1	332	4	100.0	313	2	US-08-770-554-10	Sequence 10, Appl
260	4	100.0	95	2	US-08-455-896-7	Sequence 7, Appl1	333	4	100.0	322	4	US-09-188-930-141	Sequence 141, App
261	4	100.0	95	2	US-08-933-149-7	Sequence 7, Appl1	334	4	100.0	327	4	US-09-097-767A-2	Sequence 2, Appl1
262	4	100.0	95	2	US-09-082-343-7	Sequence 7, Appl1	335	4	100.0	335	1	US-08-348-891A-4	Sequence 4, Appl1
263	4	100.0	95	3	US-09-082-353-7	Sequence 7, Appl1	336	4	100.0	335	2	US-08-905-817-4	Sequence 4, Appl1
264	4	100.0	95	3	US-08-821-451A-27	Sequence 21, Appl1	337	4	100.0	335	4	US-08-983-502-16	Sequence 16, Appl1
265	4	100.0	95	4	US-09-263-810-27	Sequence 21, Appl1	338	4	100.0	344	5	PCT-US96-10521-16	Sequence 16, Appl1
266	4	100.0	95	4	US-09-583-169-27	Sequence 27, Appl1	339	4	100.0	344	4	US-08-681-192-2	Sequence 2, Appl1
267	4	100.0	95	5	PCT-US96-08235-7	Sequence 7, Appl1	340	4	100.0	346	2	US-08-613-408B-2	Sequence 2, Appl1
268	4	100.0	97	6	5187153-8	Sequence 7, Appl1	341	4	100.0	346	2	US-08-613-220B-4	Sequence 2, Appl1
269	4	100.0	97	6	5220013-8	Patent No. 5187153	342	4	100.0	366	4	US-09-638-715-2	Sequence 4, Appl1
270	4	100.0	97	6	5223482-8	Patent No. 5223482	343	4	100.0	366	4	US-09-638-715-4	Sequence 2, Appl1
271	4	100.0	99	2	US-08-432-333-3	Sequence 3, Appl1	344	4	100.0	378	4	US-09-482-180A-2	Sequence 2, Appl1
272	4	100.0	99	3	US-08-339-708A-4	Sequence 4, Appl1	345	4	100.0	389	2	US-08-618-408B-4	Sequence 4, Appl1
273	4	100.0	99	3	US-08-339-708A-6	Sequence 6, Appl1	346	4	100.0	412	4	US-09-445-472-1	Sequence 1, Appl1
274	4	100.0	99	3	US-08-339-708A-8	Sequence 8, Appl1	347	4	100.0	421	2	US-08-484-993B-6	Sequence 6, Appl1
275	4	100.0	100	6	5187153-10	Patent No. 5187153	348	4	100.0	421	2	US-08-484-993B-24	Sequence 24, Appl1
276	4	100.0	100	6	5220013-10	Patent No. 5220013	349	4	100.0	421	2	US-08-484-158B-6	Sequence 6, Appl1
277	4	100.0	100	6	5223482-10	Patent No. 5223482	350	4	100.0	421	2	US-08-484-158B-24	Sequence 24, Appl1
278	4	100.0	101	2	US-08-242-097-6	Sequence 6, Appl1	351	4	100.0	421	2	US-08-484-158B-24	Sequence 6, Appl1
279	4	100.0	101	2	US-09-206-695-6	Sequence 6, Appl1	352	4	100.0	421	2	US-08-480-150A-6	Sequence 24, Appl1
280	4	100.0	103	2	US-08-404-831-2	Sequence 2, Appl1	353	4	100.0	421	2	US-08-480-150A-6	Sequence 24, Appl1
281	4	100.0	103	2	US-08-612-785B-2	Sequence 2, Appl1	354	4	100.0	421	2	US-08-480-150A-24	Sequence 24, Appl1
282	4	100.0	103	2	US-08-475-579A-2	Sequence 2, Appl1	355	4	100.0	421	3	US-08-458-731-6	Sequence 4, Appl1
283	4	100.0	103	2	US-08-920-162A-2	Sequence 2, Appl1	356	4	100.0	421	3	US-08-458-731-6	Sequence 4, Appl1
284	4	100.0	103	3	US-08-339-708A-10	Sequence 10, Appl1	357	4	100.0	421	3	US-08-149-223A-6	Sequence 24, Appl1
285	4	100.0	103	3	US-08-339-708A-12	Sequence 12, Appl1	358	4	100.0	421	3	US-08-149-223A-24	Sequence 24, Appl1
286	4	100.0	103	4	US-09-356-931-2	Sequence 2, Appl1	359	4	100.0	424	4	US-08-876-885-26	Sequence 26, Appl1
287	4	100.0	103	4	US-08-703-675C-2	Sequence 2, Appl1	360	4	100.0	426	2	US-08-484-993B-12	Sequence 12, Appl1
288	4	100.0	103	4	US-08-617-676C-2	Sequence 2, Appl1	361	4	100.0	426	2	US-08-484-158B-12	Sequence 12, Appl1
289	4	100.0	105	2	US-08-729-345-1	Sequence 1, Appl1	362	4	100.0	426	2	US-08-484-596A-12	Sequence 12, Appl1
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291	4	100.0	108	6	5220013-18	Patent No. 5220013	364	4	100.0	426	3	US-08-458-731-12	Sequence 12, Appl1
292	4	100.0	108	6	5223482-16	Patent No. 5223482	365	4	100.0	426	3	US-08-149-223A-12	Sequence 12, Appl1
293	4	100.0	109	4	US-09-134-001C-3523	Sequence 3523, Ap	366	4	100.0	431	4	US-09-188-930-341	Sequence 341, App
294	4	100.0	112	4	US-09-249-542-24	Sequence 24, Appl1	367	4	100.0	434	4	US-09-134-001C-4695	Sequence 4695, Ap
295	4	100.0	115	1	US-08-152-922A-7	Sequence 7, Appl1	368	4	100.0	440	4	US-09-071-035-370	Sequence 370, App
296	4	100.0	117	2	US-08-729-345-3	Sequence 3, Appl1	369	4	100.0	445	4	US-08-887-534A-61	Sequence 61, Appl
297	4	100.0	130	4	US-08-858-307A-549	Sequence 549, App	370	4	100.0	446	2	US-08-833-610-5	Sequence 5, Appl1
298	4	100.0	133	1	US-08-268-348A-8	Sequence 8, Appl1	371	4	100.0	446	3	US-08-834-033A-15	Sequence 15, Appl1
299	4	100.0	133	1	US-08-268-348A-10	Sequence 10, Appl1	372	4	100.0	448	1	US-08-366-779-5	Sequence 5, Appl1
300	4	100.0	140	4	US-09-156-388-2	Sequence 2, Appl1	373	4	100.0	448	1	US-08-789-936-5	Sequence 5, Appl1
301	4	100.0	144	4	US-08-936-165A-445	Sequence 445, App	374	4	100.0	448	4	US-08-934-254-5	Sequence 2, Appl1
302	4	100.0	163	1	US-08-469-667-11	Sequence 11, Appl1	375	4	100.0	450	4	US-09-191-879-2	Sequence 2, Appl1
303	4	100.0	163	4	US-09-224-110-11	Sequence 11, Appl1	376	4	100.0	451	4	US-09-184-963A-6	Sequence 3, Appl1
304	4	100.0	163	5	PCT-US95-07289-11	Sequence 11, Appl1	377	4	100.0	456	2	US-08-679-635A-6	Sequence 6, Appl1
305	4	100.0	167	4	US-08-959-004-7	Sequence 7, Appl1	378	4	100.0	456	4	US-09-419-163-6	Sequence 6, Appl1
306	4	100.0	181	1	US-07-949-812-8	Sequence 8, Appl1	379	4	100.0	464	5	PCT-US96-10521-18	Sequence 18, Appl1
307	4	100.0	191	4	US-09-134-001C-5345	Sequence 5345, Ap	380	4	100.0	464	5	PCT-US96-10521-18	Sequence 18, Appl1
308	4	100.0	193	2	US-08-825-780-4	Sequence 4, Appl1	381	4	100.0	472	2	US-08-622-166A-2	Sequence 2, Appl1
309	4	100.0	198	2	US-08-825-780-1	Sequence 1, Appl1	382	4	100.0	472	2	US-08-622-166A-4	Sequence 4, Appl1
310	4	100.0	198	4	US-08-825-780-3	Sequence 3, Appl1	383	4	100.0	475	4	US-09-212-247A-4	Sequence 4, Appl1
311	4	100.0	199	4	US-09-149-476-455	Sequence 455, App	384	4	100.0	476	4	US-09-561-756-27	Sequence 27, Appl1
312	4	100.0	203	2	US-08-531-525-21	Sequence 21, Appl1	385	4	100.0	476	4	US-09-227-721-27	Sequence 27, Appl1
313	4	100.0	203	4	US-08-718-270A-21	Sequence 21, Appl1	386	4	100.0	477	3	US-08-772-270A-13	Sequence 13, Appl1
314	4	100.0	203	4	US-09-134-001C-3696	Sequence 3696, Ap	387	4	100.0	479	1	US-08-665-220-2	Sequence 2, Appl1
315	4	100.0	207	2	US-08-531-525-22	Sequence 22, Appl1	388	4	100.0	479	2	US-08-807-200-12	Sequence 12, Appl1
316	4	100.0	207	2	US-08-718-270A-22	Sequence 22, Appl1	389	4	100.0	479	3	US-08-394-189B-6	Sequence 6, Appl1
317	4	100.0	224	1	US-08-265-086-4	Sequence 4, Appl1	390	4	100.0	479	3	US-08-852-782-3	Sequence 3, Appl1
318	4	100.0	227	1	US-08-265-086-2	Sequence 2, Appl1	391	4	100.0	479	4	US-09-382-155-26	Sequence 26, Appl1
319	4	100.0	227	2	US-08-801-740-5	Sequence 5, Appl1	392	4	100.0	479	4	US-09-382-155-27	Sequence 27, Appl1

393	4	100.0	479	4	US-09-382-155-28	Sequence 28, Appl	466	4	100.0	695	4	US-08-464-250-1	Sequence 1, Appl
394	4	100.0	479	4	US-09-001-777-12	Sequence 12, Appl	467	4	100.0	695	4	US-09-458-481B-4	Sequence 4, Appl
395	4	100.0	479	4	US-09-074-044A-26	Sequence 26, Appl	468	4	100.0	695	4	US-09-458-481B-5	Sequence 5, Appl
396	4	100.0	479	4	US-09-074-044A-27	Sequence 27, Appl	469	4	100.0	695	4	US-09-458-481B-6	Sequence 6, Appl
397	4	100.0	479	4	US-09-074-044A-28	Sequence 28, Appl	470	4	100.0	695	4	US-09-458-481B-7	Sequence 7, Appl
398	4	100.0	479	4	US-09-291-522-2	Sequence 2, Appl	471	4	100.0	695	4	US-09-458-481B-8	Sequence 8, Appl
399	4	100.0	479	4	US-09-561-756-33	Sequence 33, Appl	472	4	100.0	695	4	US-09-548-372D-10	Sequence 10, Appl
400	4	100.0	479	4	US-09-227-721-33	Sequence 33, Appl	473	4	100.0	695	4	US-09-548-372D-12	Sequence 12, Appl
401	4	100.0	479	4	US-08-983-502-7	Sequence 7, Appl	474	4	100.0	695	4	US-09-548-372D-14	Sequence 14, Appl
402	4	100.0	479	5	PCT-US96-10521-7	Sequence 4, Appl	475	4	100.0	695	4	US-09-548-367D-10	Sequence 10, Appl
403	4	100.0	480	4	US-08-965-902A-4	Sequence 4, Appl	476	4	100.0	695	4	US-09-548-367D-12	Sequence 12, Appl
404	4	100.0	480	5	PCT-US93-05701-21	Sequence 21, Appl	477	4	100.0	695	4	US-09-548-367D-14	Sequence 14, Appl
405	4	100.0	480	5	PCT-US93-05705-6	Sequence 6, Appl	478	4	100.0	695	5	PCT-US94-01712-27	Sequence 27, Appl
406	4	100.0	487	1	US-08-462-859A-9	Sequence 9, Appl	479	4	100.0	695	6	5218100-2	Patent No. 5218100
407	4	100.0	487	1	US-08-123-659A-9	Sequence 9, Appl	480	4	100.0	697	4	US-09-548-372D-16	Sequence 16, Appl
408	4	100.0	487	1	US-08-464-247A-9	Sequence 9, Appl	481	4	100.0	697	4	US-09-548-372D-18	Sequence 18, Appl
409	4	100.0	487	1	US-08-464-248A-9	Sequence 9, Appl	482	4	100.0	697	4	US-09-548-372D-20	Sequence 20, Appl
410	4	100.0	492	1	US-08-462-859A-7	Sequence 7, Appl	483	4	100.0	697	4	US-09-548-367D-16	Sequence 16, Appl
411	4	100.0	492	1	US-08-123-659A-7	Sequence 7, Appl	484	4	100.0	697	4	US-09-548-367D-18	Sequence 18, Appl
412	4	100.0	492	1	US-08-464-247A-7	Sequence 7, Appl	485	4	100.0	697	4	US-09-548-367D-20	Sequence 20, Appl
413	4	100.0	492	1	US-08-464-248A-7	Sequence 7, Appl	486	4	100.0	698	1	US-08-376-362A-20	Sequence 20, Appl
414	4	100.0	496	1	US-08-665-220-4	Sequence 4, Appl	487	4	100.0	702	4	US-09-653-839-6	Sequence 6, Appl
415	4	100.0	496	4	US-09-291-592-4	Sequence 4, Appl	488	4	100.0	708	1	US-08-396-479B-8	Sequence 8, Appl
416	4	100.0	497	3	US-08-258-287B-37	Sequence 37, Appl	489	4	100.0	708	2	US-08-818-823-8	Sequence 8, Appl
417	4	100.0	497	3	US-08-368-704C-37	Sequence 37, Appl	490	4	100.0	708	2	US-08-655-640-4	Sequence 4, Appl
418	4	100.0	503	3	US-08-258-287B-36	Sequence 36, Appl	491	4	100.0	711	1	US-08-145-681-2	Sequence 2, Appl
419	4	100.0	503	3	US-08-368-704C-36	Sequence 36, Appl	492	4	100.0	711	1	US-08-250-308-2	Sequence 2, Appl
420	4	100.0	505	2	US-08-394-189B-5	Sequence 5, Appl	493	4	100.0	711	1	US-08-154-019-4	Sequence 4, Appl
421	4	100.0	505	5	PCT-US93-05701-20	Sequence 20, Appl	494	4	100.0	711	1	US-08-461-333-4	Sequence 4, Appl
422	4	100.0	505	5	PCT-US93-05705-5	Sequence 5, Appl	495	4	100.0	711	1	US-08-453-703-2	Sequence 2, Appl
423	4	100.0	506	2	US-08-659-984A-21	Sequence 21, Appl	496	4	100.0	711	2	US-08-456-106-2	Sequence 2, Appl
424	4	100.0	506	4	US-08-660-531-21	Sequence 21, Appl	497	4	100.0	711	3	US-08-464-167-4	Sequence 4, Appl
425	4	100.0	506	4	US-09-054-334-4	Sequence 4, Appl	498	4	100.0	711	3	US-09-158-313-4	Sequence 4, Appl
426	4	100.0	522	4	US-08-894-818B-3	Sequence 3, Appl	499	4	100.0	711	3	US-08-456-108-2	Sequence 2, Appl
427	4	100.0	522	4	US-09-445-472-4	Sequence 4, Appl	500	4	100.0	711	4	US-08-476-798-4	Sequence 4, Appl
428	4	100.0	537	1	US-08-453-552-4	Sequence 4, Appl	501	4	100.0	711	4	US-09-265-577-2	Sequence 2, Appl
429	4	100.0	537	2	US-08-710-637-4	Sequence 4, Appl	502	4	100.0	711	5	PCT-US93-03614-2	Sequence 2, Appl
430	4	100.0	537	5	PCT-US93-00907-4	Sequence 4, Appl	503	4	100.0	714	4	US-09-422-869-22	Sequence 22, Appl
431	4	100.0	546	4	US-09-134-001C-3903	Sequence 3903, Ap	504	4	100.0	723	4	US-09-653-839-4	Sequence 4, Appl
432	4	100.0	549	3	US-08-886-886C-13	Sequence 13, Appl	505	4	100.0	734	4	US-09-532-594B-4	Sequence 4, Appl
433	4	100.0	549	4	US-09-693-146-2	Sequence 2, Appl	506	4	100.0	739	1	US-08-396-479B-10	Sequence 10, Appl
434	4	100.0	566	4	US-09-073-297-5	Sequence 5, Appl	507	4	100.0	739	1	US-08-818-823-10	Sequence 10, Appl
435	4	100.0	571	4	US-09-071-035-168	Sequence 168, App	508	4	100.0	739	4	US-09-653-839-2	Sequence 2, Appl
436	4	100.0	584	4	US-09-022-949-2	Sequence 2, Appl	509	4	100.0	740	4	US-09-323-872A-23	Sequence 23, Appl
437	4	100.0	586	3	US-08-419-810-12	Sequence 12, Appl	510	4	100.0	751	1	US-08-123-702-4	Sequence 4, Appl
438	4	100.0	586	6	5405775-11	Patent No. 5405775	511	4	100.0	751	2	US-08-104-165-2	Sequence 2, Appl
439	4	100.0	593	4	US-09-071-035-166	Sequence 166, App	512	4	100.0	751	2	US-08-422-333-2	Sequence 2, Appl
440	4	100.0	598	4	US-09-532-594B-16	Sequence 16, Appl	513	4	100.0	751	3	US-08-422-333-21	Sequence 21, Appl
441	4	100.0	599	4	US-09-357-251-14	Sequence 14, Appl	514	4	100.0	751	3	US-08-464-250-2	Sequence 2, Appl
442	4	100.0	613	1	US-08-272-875-3	Sequence 3, Appl	515	4	100.0	751	4	US-08-464-250-2	Sequence 2, Appl
443	4	100.0	616	4	US-08-965-902A-2	Sequence 2, Appl	516	4	100.0	751	4	US-08-832-867-5	Sequence 5, Appl
444	4	100.0	618	4	US-08-595-553A-2	Sequence 2, Appl	517	4	100.0	751	4	US-09-548-372D-57	Sequence 57, Appl
445	4	100.0	625	4	US-09-134-001C-4504	Sequence 4504, Ap	518	4	100.0	751	4	US-09-548-367D-57	Sequence 57, Appl
446	4	100.0	626	4	US-09-134-001C-4342	Sequence 4342, Ap	519	4	100.0	751	6	5187153-2	Patent No. 5187153
447	4	100.0	628	1	US-08-237-073-9	Sequence 9, Appl	520	4	100.0	751	6	5220013-2	Patent No. 5220013
448	4	100.0	654	4	US-08-894-818B-35	Sequence 35, Appl	521	4	100.0	751	6	5223482-2	Patent No. 5223482
449	4	100.0	654	4	US-09-445-472-16	Sequence 16, Appl	522	4	100.0	753	4	US-09-548-372D-61	Sequence 61, Appl
450	4	100.0	655	4	US-09-228-986-70	Sequence 70, Appl	523	4	100.0	753	4	US-09-548-367D-61	Sequence 61, Appl
451	4	100.0	656	1	US-08-371-930-23	Sequence 23, Appl	524	4	100.0	770	1	US-08-133-248-8	Sequence 8, Appl
452	4	100.0	656	5	PCT-US94-01712-23	Sequence 23, Appl	525	4	100.0	770	1	US-08-231-940-1	Sequence 1, Appl
453	4	100.0	676	1	US-08-371-930-24	Sequence 24, Appl	526	4	100.0	770	2	US-08-641-774-1	Sequence 1, Appl
454	4	100.0	676	5	PCT-US94-01712-24	Sequence 24, Appl	527	4	100.0	770	2	US-08-104-165-3	Sequence 3, Appl
455	4	100.0	686	4	US-09-653-839A-8	Sequence 8, Appl	528	4	100.0	770	3	US-08-464-250-3	Sequence 3, Appl
456	4	100.0	694	1	US-08-339-152A-18	Sequence 18, Appl	529	4	100.0	770	4	US-08-464-250-3	Sequence 3, Appl
457	4	100.0	694	2	US-08-007-999B-5	Sequence 5, Appl	530	4	100.0	770	4	US-09-548-372D-55	Sequence 55, Appl
458	4	100.0	694	2	US-08-895-522-4	Sequence 4, Appl	531	4	100.0	770	4	US-09-548-367D-55	Sequence 55, Appl
459	4	100.0	694	2	US-08-689-276A-5	Sequence 5, Appl	532	4	100.0	772	4	US-09-548-372D-59	Sequence 59, Appl
460	4	100.0	694	3	US-09-195-391-4	Sequence 4, Appl	533	4	100.0	772	4	US-09-548-367D-59	Sequence 59, Appl
461	4	100.0	695	1	US-08-371-930-27	Sequence 27, Appl	534	4	100.0	806	4	US-08-945-983-2	Sequence 2, Appl
462	4	100.0	695	1	US-08-123-702-2	Sequence 2, Appl	535	4	100.0	810	4	US-09-323-872A-29	Sequence 29, Appl
463	4	100.0	695	1	US-08-339-152A-30	Sequence 30, Appl	536	4	100.0	834	1	US-08-491-357-2	Sequence 2, Appl
464	4	100.0	695	2	US-08-104-165-1	Sequence 1, Appl	537	4	100.0	834	3	US-08-968-633-2	Sequence 2, Appl
465	4	100.0	695	3	US-08-464-250-1	Sequence 1, Appl	538	4	100.0	834	3	US-09-196-466-2	Sequence 2, Appl



539	4	100.0	834	5	PCT-US96-10823-2	Sequence 2, Appl1	612	3	75.0	4	4	US-08-617-267C-12	Sequence 12, Appl1
540	4	100.0	863	2	US-08-666-871-2	Sequence 28, Appl1	613	3	75.0	4	4	US-09-095-106A-24	Sequence 24, Appl1
541	4	100.0	864	4	US-09-323-872A-28	Sequence 3, Appl1	614	3	75.0	4	4	US-09-095-106A-26	Sequence 26, Appl1
542	4	100.0	872	1	US-08-491-357-3	Sequence 3, Appl1	615	3	75.0	4	4	US-09-664-295-27	Sequence 27, Appl1
543	4	100.0	872	3	US-08-968-633-3	Sequence 3, Appl1	616	3	75.0	4	5	PCT-US91-06950-92	Sequence 92, Appl1
544	4	100.0	872	3	US-09-196-466-3	Sequence 3, Appl1	617	3	75.0	5	1	US-07-690-288A-15	Sequence 15, Appl1
545	4	100.0	872	5	PCT-US96-10823-3	Sequence 3, Appl1	618	3	75.0	5	2	US-08-612-785B-11	Sequence 11, Appl1
546	4	100.0	876	4	US-09-254-352B-19	Sequence 19, Appl1	619	3	75.0	5	2	US-08-612-785B-12	Sequence 12, Appl1
547	4	100.0	902	1	US-08-396-479B-6	Sequence 6, Appl1	620	3	75.0	5	2	US-08-612-785B-26	Sequence 26, Appl1
548	4	100.0	902	1	US-08-818-823-6	Sequence 6, Appl1	621	3	75.0	5	2	US-08-612-785B-30	Sequence 30, Appl1
549	4	100.0	1024	4	US-09-522-666-2	Sequence 2, Appl1	622	3	75.0	5	2	US-08-612-785B-32	Sequence 32, Appl1
550	4	100.0	1024	4	US-09-562-737-87	Sequence 87, Appl1	623	3	75.0	5	2	US-08-920-162A-3	Sequence 3, Appl1
551	4	100.0	1068	1	US-08-396-479B-12	Sequence 12, Appl1	624	3	75.0	5	2	US-08-920-162A-16	Sequence 16, Appl1
552	4	100.0	1068	1	US-08-818-823-12	Sequence 12, Appl1	625	3	75.0	5	2	US-08-920-162A-20	Sequence 20, Appl1
553	4	100.0	1075	5	PCT-US94-07297-41	Sequence 41, Appl1	626	3	75.0	5	2	US-08-920-162A-21	Sequence 21, Appl1
554	4	100.0	1101	4	US-09-770-170-8	Sequence 8, Appl1	627	3	75.0	5	2	US-08-920-162A-27	Sequence 27, Appl1
555	4	100.0	1140	4	US-09-651-656-21	Sequence 21, Appl1	628	3	75.0	5	2	US-08-920-162A-38	Sequence 38, Appl1
556	4	100.0	1140	4	US-09-650-855-21	Sequence 21, Appl1	629	3	75.0	5	2	US-08-920-162A-33	Sequence 33, Appl1
557	4	100.0	1263	4	US-09-351-824E-11	Sequence 11, Appl1	630	3	75.0	5	2	US-08-920-162A-34	Sequence 34, Appl1
558	4	100.0	1333	4	US-09-347-878-20	Sequence 20, Appl1	631	3	75.0	5	2	US-09-188-579-52	Sequence 52, Appl1
559	4	100.0	1693	3	US-08-840-316-1	Sequence 1, Appl1	632	3	75.0	5	4	US-09-315-444-52	Sequence 52, Appl1
560	4	100.0	1693	3	US-08-478-507-7	Sequence 7, Appl1	633	3	75.0	5	4	US-08-341-555-8	Sequence 8, Appl1
561	4	100.0	1693	4	US-08-809-523-1	Sequence 1, Appl1	634	3	75.0	5	4	US-09-356-931-3	Sequence 3, Appl1
562	4	100.0	1693	4	US-09-128-275A-7	Sequence 7, Appl1	635	3	75.0	5	4	US-09-356-931-16	Sequence 16, Appl1
563	4	100.0	1693	4	US-08-471-971-1	Sequence 1, Appl1	636	3	75.0	5	4	US-09-356-931-20	Sequence 20, Appl1
564	4	100.0	1693	4	US-09-553-427-7	Sequence 7, Appl1	637	3	75.0	5	4	US-09-356-931-21	Sequence 21, Appl1
565	4	100.0	1693	4	US-09-402-776-1	Sequence 1, Appl1	638	3	75.0	5	4	US-09-356-931-27	Sequence 27, Appl1
566	4	100.0	1693	5	PCT-US93-08849A-1	Sequence 1, Appl1	639	3	75.0	5	4	US-09-356-931-28	Sequence 28, Appl1
567	4	100.0	1693	5	PCT-US93-08849-1	Sequence 1, Appl1	640	3	75.0	5	4	US-09-356-931-33	Sequence 33, Appl1
568	4	100.0	1708	3	US-09-462-606-2	Sequence 2, Appl1	641	3	75.0	5	4	US-09-356-931-34	Sequence 34, Appl1
569	4	100.0	1713	3	US-08-600-982-24	Sequence 24, Appl1	642	3	75.0	5	4	US-08-703-675C-10	Sequence 10, Appl1
570	4	100.0	1713	5	PCT-US94-10261A-24	Sequence 24, Appl1	643	3	75.0	5	4	US-08-703-675C-16	Sequence 16, Appl1
571	4	100.0	1727	2	US-08-477-451-10	Sequence 10, Appl1	644	3	75.0	5	4	US-08-703-675C-20	Sequence 20, Appl1
572	4	100.0	1865	1	US-08-588-985-2	Sequence 2, Appl1	645	3	75.0	5	4	US-08-617-267C-32	Sequence 32, Appl1
573	4	100.0	1865	1	US-08-971-988-2	Sequence 2, Appl1	646	3	75.0	5	4	US-08-617-267C-36	Sequence 36, Appl1
574	4	100.0	1871	2	US-08-694-869-1	Sequence 1, Appl1	647	3	75.0	5	4	US-08-617-267C-30	Sequence 30, Appl1
575	4	100.0	1871	3	US-09-449-546-1	Sequence 1, Appl1	648	3	75.0	5	4	US-08-703-675C-39	Sequence 39, Appl1
576	4	100.0	1881	4	US-09-233-086-3	Sequence 3, Appl1	649	3	75.0	5	4	US-08-703-675C-45	Sequence 45, Appl1
577	4	100.0	2289	3	US-09-051-019-2	Sequence 2, Appl1	650	3	75.0	5	4	US-08-617-267C-11	Sequence 11, Appl1
578	4	100.0	2938	5	PCT-US94-00198-3	Sequence 3, Appl1	651	3	75.0	5	4	US-08-617-267C-32	Sequence 32, Appl1
579	3	75.0		3	US-08-920-162A-10	Sequence 10, Appl1	652	3	75.0	5	4	US-08-617-267C-36	Sequence 36, Appl1
580	3	75.0		3	US-09-356-931-10	Sequence 10, Appl1	653	3	75.0	5	4	US-08-617-267C-30	Sequence 30, Appl1
581	3	75.0		3	US-08-703-675C-10	Sequence 10, Appl1	654	3	75.0	5	4	US-08-617-267C-32	Sequence 32, Appl1
582	3	75.0		3	US-09-095-106A-32	Sequence 32, Appl1	655	3	75.0	5	4	US-08-617-267C-11	Sequence 11, Appl1
583	3	75.0		3	US-09-095-106A-33	Sequence 33, Appl1	656	3	75.0	5	4	US-09-095-106A-20	Sequence 20, Appl1
584	3	75.0		4	US-08-451-947-92	Sequence 92, Appl1	657	3	75.0	5	4	US-09-095-106A-39	Sequence 39, Appl1
585	3	75.0		4	US-08-304-585-10	Sequence 10, Appl1	658	3	75.0	5	4	US-09-095-106A-42	Sequence 42, Appl1
586	3	75.0		4	US-08-387-156-24	Sequence 24, Appl1	659	3	75.0	5	4	US-09-721-165-72	Sequence 72, Appl1
587	3	75.0		4	US-08-424-826A-92	Sequence 92, Appl1	660	3	75.0	5	4	US-08-766-596A-30	Sequence 30, Appl1
588	3	75.0		4	US-08-694-865-30	Sequence 30, Appl1	661	3	75.0	5	4	US-08-766-596A-32	Sequence 32, Appl1
589	3	75.0		4	US-08-612-785B-12	Sequence 12, Appl1	662	3	75.0	5	4	US-08-612-785B-27	Sequence 27, Appl1
590	3	75.0		4	US-08-685-589A-30	Sequence 30, Appl1	663	3	75.0	6	1	US-07-943-709-63	Sequence 63, Appl1
591	3	75.0		4	US-08-878-748-24	Sequence 24, Appl1	664	3	75.0	6	2	US-08-612-785B-27	Sequence 27, Appl1
592	3	75.0		4	US-08-920-162A-8	Sequence 8, Appl1	665	3	75.0	6	4	US-08-703-675C-40	Sequence 40, Appl1
593	3	75.0		4	US-08-920-162A-9	Sequence 9, Appl1	666	3	75.0	6	4	US-08-617-267C-11	Sequence 11, Appl1
594	3	75.0		4	US-08-920-162A-13	Sequence 13, Appl1	667	3	75.0	6	4	US-09-095-106A-16	Sequence 16, Appl1
595	3	75.0		4	US-08-920-162A-14	Sequence 14, Appl1	668	3	75.0	6	6	5252328-11	Patent No. 5252328
596	3	75.0		4	US-08-920-162A-15	Sequence 15, Appl1	669	3	75.0	7	1	US-08-397-633A-105	Sequence 105, App
597	3	75.0		4	US-09-124-491-30	Sequence 30, Appl1	670	3	75.0	7	1	US-08-220-401-18	Sequence 18, Appl1
598	3	75.0		4	US-08-928-694-92	Sequence 92, Appl1	671	3	75.0	7	2	US-08-437-362-18	Sequence 18, Appl1
599	3	75.0		4	US-08-581-662-27	Sequence 27, Appl1	672	3	75.0	7	2	US-08-510-215A-7	Sequence 7, Appl1
600	3	75.0		4	US-08-341-555-9	Sequence 9, Appl1	673	3	75.0	7	2	US-08-441-513A-19	Sequence 19, Appl1
601	3	75.0		4	US-09-356-931-8	Sequence 8, Appl1	674	3	75.0	7	4	US-09-173-941-11	Sequence 11, Appl1
602	3	75.0		4	US-09-356-931-9	Sequence 9, Appl1	675	3	75.0	7	4	US-09-173-941-65	Sequence 65, Appl1
603	3	75.0		4	US-09-356-931-13	Sequence 13, Appl1	676	3	75.0	7	4	US-09-173-941-75	Sequence 75, Appl1
604	3	75.0		4	US-09-356-931-14	Sequence 14, Appl1	677	3	75.0	7	4	US-09-258-754-236	Sequence 236, App
605	3	75.0		4	US-09-356-931-15	Sequence 15, Appl1	678	3	75.0	7	4	US-09-169-015-15	Sequence 15, Appl1
606	3	75.0		4	US-08-703-675C-8	Sequence 8, Appl1	679	3	75.0	7	4	US-09-042-107-266	Sequence 266, App
607	3	75.0		4	US-08-703-675C-9	Sequence 9, Appl1	680	3	75.0	7	4	US-09-095-106A-13	Sequence 13, Appl1
608	3	75.0		4	US-08-703-675C-13	Sequence 13, Appl1	681	3	75.0	7	4	US-08-255-208A-40	Sequence 40, Appl1
609	3	75.0		4	US-08-703-675C-14	Sequence 14, Appl1	682	3	75.0	7	6	5510256-1	Patent No. 5510256
610	3	75.0		4	US-08-703-675C-15	Sequence 15, Appl1	683	3	75.0	8	1	US-08-457-804-4	Sequence 4, Appl1
611	3	75.0		4	US-09-242-724-29	Sequence 29, Appl1	684	3	75.0	8	1	US-08-457-804-5	Sequence 5, Appl1

685	3	75.0	8	1	US-08-457-804-11	Sequence 11, Appl	758	3	75.0	10	3	US-08-159-339A-547	Sequence 547, App
686	3	75.0	8	1	US-08-457-804-13	Sequence 13, Appl	759	3	75.0	10	3	US-08-159-339A-1031	Sequence 1031, Ap
687	3	75.0	8	1	US-08-457-804-14	Sequence 14, Appl	760	3	75.0	10	3	US-08-667-725B-5	Sequence 5, Appli
688	3	75.0	8	2	US-08-682-245A-5	Sequence 5, Appli	761	3	75.0	10	3	US-08-195-006-10	Sequence 10, Appl
689	3	75.0	8	2	US-08-595-043A-42	Sequence 42, Appl	762	3	75.0	10	3	US-09-037-190-30	Sequence 30, Appl
690	3	75.0	8	4	US-08-706-344C-20	Sequence 20, Appl	763	3	75.0	10	3	US-09-037-192-30	Sequence 30, Appl
691	3	75.0	8	4	US-09-095-106A-10	Sequence 10, Appl	764	3	75.0	10	4	US-09-007-748-5	Sequence 5, Appli
692	3	75.0	8	4	US-08-255-208A-41	Sequence 41, Appl	765	3	75.0	10	4	US-09-037-143-30	Sequence 30, Appl
693	3	75.0	9	1	US-08-217-188A-6	Sequence 6, Appli	766	3	75.0	10	4	US-09-049-691-30	Sequence 30, Appl
694	3	75.0	9	1	US-08-299-849B-6	Sequence 6, Appli	767	3	75.0	10	4	US-08-260-174-30	Sequence 30, Appl
695	3	75.0	9	1	US-08-462-128-9	Sequence 9, Appli	768	3	75.0	10	4	US-09-183-931-32	Sequence 32, Appl
696	3	75.0	9	1	US-08-462-128-9	Sequence 9, Appli	769	3	75.0	10	4	US-09-061-388-20	Sequence 20, Appl
697	3	75.0	9	1	US-08-462-128-10	Sequence 10, Appl	770	3	75.0	10	4	US-09-227-693-41	Sequence 41, Appl
698	3	75.0	9	1	US-08-462-128-11	Sequence 11, Appl	771	3	75.0	10	4	US-09-338-128A-30	Sequence 30, Appl
699	3	75.0	9	1	US-08-462-128-28	Sequence 28, Appl	772	3	75.0	10	4	US-09-099-543C-20	Sequence 20, Appl
700	3	75.0	9	1	US-08-462-128-33	Sequence 33, Appl	773	3	75.0	10	4	US-09-516-914-41	Sequence 41, Appl
701	3	75.0	9	1	US-08-687-226-6	Sequence 6, Appli	774	3	75.0	10	4	US-09-516-914-42	Sequence 42, Appl
702	3	75.0	9	1	US-08-464-318-6	Sequence 6, Appli	775	3	75.0	10	4	US-09-232-346-30	Sequence 30, Appl
703	3	75.0	9	1	US-08-463-180-7	Sequence 7, Appli	776	3	75.0	10	4	US-09-705-160-32	Sequence 32, Appl
704	3	75.0	9	1	US-08-463-180-9	Sequence 9, Appli	777	3	75.0	10	4	US-09-037-179-30	Sequence 30, Appl
705	3	75.0	9	1	US-08-463-180-10	Sequence 10, Appl	778	3	75.0	10	4	US-09-257-179-73	Sequence 73, Appl
706	3	75.0	9	1	US-08-463-180-11	Sequence 11, Appl	779	3	75.0	10	4	US-08-197-484-83	Sequence 83, Appl
707	3	75.0	9	1	US-08-463-180-28	Sequence 28, Appl	780	3	75.0	10	4	US-08-197-484-142	Sequence 142, App
708	3	75.0	9	1	US-08-463-180-33	Sequence 33, Appl	781	3	75.0	10	4	US-08-255-208A-43	Sequence 43, Appl
709	3	75.0	9	1	US-08-615-181-44	Sequence 44, Appl	782	3	75.0	10	5	PCT-US94-07644A-10	Sequence 10, Appl
710	3	75.0	9	2	US-08-471-341-6	Sequence 6, Appli	783	3	75.0	10	5	PCT-US95-02121-83	Sequence 83, Appl
711	3	75.0	9	2	US-08-461-566-6	Sequence 6, Appli	784	3	75.0	10	5	PCT-US95-02121-142	Sequence 142, App
712	3	75.0	9	2	US-08-142-368A-6	Sequence 6, Appli	785	3	75.0	11	1	US-08-217-188A-7	Sequence 7, Appli
713	3	75.0	9	2	US-08-537-400-23	Sequence 23, Appl	786	3	75.0	11	1	US-08-217-188A-25	Sequence 25, Appl
714	3	75.0	9	2	US-08-986-234-60	Sequence 60, Appl	787	3	75.0	11	1	US-08-687-226-7	Sequence 7, Appli
715	3	75.0	9	3	US-08-967-727-6	Sequence 6, Appli	788	3	75.0	11	1	US-08-687-226-25	Sequence 25, Appl
716	3	75.0	9	3	US-08-159-339A-98	Sequence 98, Appl	789	3	75.0	11	1	US-08-388-267C-11	Sequence 11, Appl
717	3	75.0	9	3	US-08-159-339A-435	Sequence 435, App	790	3	75.0	11	1	US-08-428-415-31	Sequence 31, Appl
718	3	75.0	9	3	US-08-159-339A-1008	Sequence 1008, Ap	791	3	75.0	11	1	US-08-379-685-31	Sequence 31, Appl
719	3	75.0	9	3	US-08-159-339A-1009	Sequence 1009, Ap	792	3	75.0	11	2	US-08-248-839C-59	Sequence 59, Appl
720	3	75.0	9	3	US-08-159-339A-1210	Sequence 1210, Ap	793	3	75.0	11	2	US-08-854-029-31	Sequence 31, Appl
721	3	75.0	9	3	US-08-667-725B-6	Sequence 6, Appli	794	3	75.0	11	3	US-08-159-339A-1143	Sequence 1143, Ap
722	3	75.0	9	3	US-08-064-964-2	Sequence 2, Appli	795	3	75.0	11	3	US-08-667-725B-7	Sequence 7, Appli
723	3	75.0	9	3	US-09-188-579-91	Sequence 91, Appl	796	3	75.0	11	3	US-08-667-725B-25	Sequence 25, Appl
724	3	75.0	9	4	US-09-007-748-6	Sequence 6, Appli	797	3	75.0	11	4	US-09-007-748-7	Sequence 7, Appli
725	3	75.0	9	4	US-09-315-444-91	Sequence 91, Appl	798	3	75.0	11	4	US-09-007-748-25	Sequence 25, Appl
726	3	75.0	9	4	US-08-037-230D-6	Sequence 6, Appli	799	3	75.0	11	4	US-08-428-762-31	Sequence 31, Appl
727	3	75.0	9	4	US-08-518-046-47	Sequence 47, Appl	800	3	75.0	11	4	US-09-277-720-11	Sequence 11, Appl
728	3	75.0	9	4	US-09-518-046-122	Sequence 122, App	801	3	75.0	11	4	US-08-255-208A-44	Sequence 44, Appl
729	3	75.0	9	4	US-09-518-046-146	Sequence 146, App	802	3	75.0	12	1	US-08-302-808-11	Sequence 11, Appl
730	3	75.0	9	4	US-09-052-521C-40	Sequence 40, Appl	803	3	75.0	12	2	US-08-146-028-5	Sequence 5, Appli
731	3	75.0	9	4	US-09-064-174-2	Sequence 2, Appli	804	3	75.0	12	2	US-08-986-948-11	Sequence 11, Appl
732	3	75.0	9	4	US-09-053-611-4	Sequence 4, Appli	805	3	75.0	12	2	US-08-726-306A-136	Sequence 136, App
733	3	75.0	9	4	US-09-721-362-91	Sequence 91, Appl	806	3	75.0	12	3	US-08-792-832A-9	Sequence 9, Appli
734	3	75.0	9	4	US-08-255-208A-42	Sequence 42, Appl	807	3	75.0	12	3	US-08-466-368-11	Sequence 11, Appl
735	3	75.0	9	4	US-08-766-596A-52	Sequence 52, Appl	808	3	75.0	12	3	US-09-188-579-9	Sequence 9, Appli
736	3	75.0	9	5	PCT-US95-16415-38	Sequence 38, Appl	809	3	75.0	12	4	US-09-060-039-3	Sequence 3, Appli
737	3	75.0	9	6	5428007-3	Patent No. 5428007	810	3	75.0	12	4	US-09-060-039-4	Sequence 4, Appli
738	3	75.0	10	1	US-08-217-188A-5	Sequence 5, Appli	811	3	75.0	12	4	US-09-060-039-5	Sequence 5, Appli
739	3	75.0	10	1	US-08-331-398A-41	Sequence 41, Appl	812	3	75.0	12	4	US-09-060-039-6	Sequence 6, Appli
740	3	75.0	10	1	US-08-462-128-1	Sequence 1, Appli	813	3	75.0	12	4	US-09-060-039-7	Sequence 7, Appli
741	3	75.0	10	1	US-08-462-128-2	Sequence 2, Appli	814	3	75.0	12	4	US-09-060-039-11	Sequence 11, Appl
742	3	75.0	10	1	US-08-462-128-3	Sequence 3, Appli	815	3	75.0	12	4	US-09-060-039-12	Sequence 12, Appl
743	3	75.0	10	1	US-08-462-128-4	Sequence 4, Appli	816	3	75.0	12	4	US-09-060-039-13	Sequence 13, Appl
744	3	75.0	10	1	US-08-462-128-42	Sequence 42, Appl	817	3	75.0	12	4	US-09-060-039-14	Sequence 14, Appl
745	3	75.0	10	1	US-08-462-128-43	Sequence 43, Appl	818	3	75.0	12	4	US-09-060-039-15	Sequence 15, Appl
746	3	75.0	10	1	US-08-687-226-5	Sequence 5, Appli	819	3	75.0	12	4	US-09-060-039-18	Sequence 18, Appl
747	3	75.0	10	1	US-08-214-650-28	Sequence 28, Appl	820	3	75.0	12	4	US-09-060-039-19	Sequence 19, Appl
748	3	75.0	10	1	US-08-463-180-1	Sequence 1, Appli	821	3	75.0	12	4	US-09-060-039-21	Sequence 21, Appl
749	3	75.0	10	1	US-08-463-180-2	Sequence 2, Appli	822	3	75.0	12	4	US-09-060-039-22	Sequence 22, Appl
750	3	75.0	10	1	US-08-463-180-3	Sequence 3, Appli	823	3	75.0	12	4	US-08-723-425A-5	Sequence 5, Appli
751	3	75.0	10	1	US-08-463-180-4	Sequence 4, Appli	824	3	75.0	12	4	US-09-112-206-5	Sequence 5, Appli
752	3	75.0	10	1	US-08-463-180-42	Sequence 42, Appl	825	3	75.0	12	4	US-09-177-249-8	Sequence 8, Appli
753	3	75.0	10	1	US-08-463-180-43	Sequence 43, Appl	826	3	75.0	12	4	US-09-315-444-9	Sequence 9, Appli
754	3	75.0	10	2	US-08-902-623-71	Sequence 71, Appl	827	3	75.0	12	4	US-09-001-984C-75	Sequence 75, Appl
755	3	75.0	10	2	US-08-331-397B-41	Sequence 41, Appl	828	3	75.0	12	4	US-09-721-362-9	Sequence 9, Appli
756	3	75.0	10	2	US-08-759-804A-41	Sequence 41, Appl	829	3	75.0	12	4	US-08-255-208A-45	Sequence 45, Appl
757	3	75.0	10	3	US-08-592-500-10	Sequence 10, Appl	830	3	75.0	12	4	US-09-752-165-11	Sequence 11, Appl

831	3	75.0	12	6	5443956-2	Patent No. 5443956	904	3	75.0	16	2	US-08-956-266-4	Sequence 4, Appl
832	3	75.0	12	6	5443956-3	Patent No. 5443956	905	3	75.0	16	2	US-08-928-615-6	Sequence 6, Appl
833	3	75.0	12	6	5443956-4	Patent No. 5443956	906	3	75.0	16	2	US-08-478-572-185	Sequence 185, App
834	3	75.0	12	6	5443956-7	Patent No. 5443956	907	3	75.0	16	2	US-08-478-572-186	Sequence 186, App
835	3	75.0	13	1	US-07-977-672-7	Sequence 7, Appl	908	3	75.0	16	2	US-08-484-905-45	Sequence 45, Appl
836	3	75.0	13	1	US-08-368-267C-12	Sequence 12, Appl	909	3	75.0	16	3	US-08-481-985B-45	Sequence 45, Appl
837	3	75.0	13	4	US-09-286-959B-7	Sequence 7, Appl	910	3	75.0	16	3	US-09-093-522-4	Sequence 4, Appl
838	3	75.0	13	4	US-09-217-720-12	Sequence 12, Appl	911	3	75.0	16	4	US-09-171-705-1	Sequence 45, Appl
839	3	75.0	13	4	US-08-822-940-7	Sequence 7, Appl	912	3	75.0	16	4	US-09-171-705-38	Sequence 38, Appl
840	3	75.0	13	4	US-08-255-208A-46	Sequence 46, Appl	913	3	75.0	16	4	US-09-171-705-39	Sequence 39, Appl
841	3	75.0	13	5	PCT-US94-10257A-14	Sequence 14, Appl	914	3	75.0	16	4	US-09-177-249-291	Sequence 291, Appl
842	3	75.0	13	5	PCT-US94-10257A-58	Sequence 58, Appl	915	3	75.0	16	4	US-09-248-588-80	Sequence 80, Appl
843	3	75.0	13	5	PCT-US94-10257A-59	Sequence 59, Appl	916	3	75.0	16	4	US-08-484-296-185	Sequence 185, App
844	3	75.0	13	5	PCT-US94-10257A-60	Sequence 60, Appl	917	3	75.0	16	4	US-08-484-296-186	Sequence 186, App
845	3	75.0	13	5	PCT-US94-10257A-61	Sequence 61, Appl	918	3	75.0	16	4	US-09-166-448-6	Sequence 6, Appl
846	3	75.0	13	5	PCT-US94-10257A-62	Sequence 62, Appl	919	3	75.0	16	4	US-08-992-877-25	Sequence 25, Appl
847	3	75.0	13	6	5210180-2	Patent No. 5210180	920	3	75.0	16	4	US-09-348-933-6	Sequence 6, Appl
848	3	75.0	14	1	US-07-908-317-31	Sequence 31, Appl	921	3	75.0	16	4	US-08-828-323-16	Sequence 16, Appl
849	3	75.0	14	1	US-08-036-555B-126	Sequence 126, App	922	3	75.0	16	4	US-09-697-884-6	Sequence 6, Appl
850	3	75.0	14	1	US-08-469-569-126	Sequence 126, App	923	3	75.0	16	4	US-08-828-323-16	Sequence 16, Appl
851	3	75.0	14	1	US-08-222-619-31	Sequence 31, Appl	924	3	75.0	16	4	US-08-255-208A-49	Sequence 49, Appl
852	3	75.0	14	1	US-08-249-322A-126	Sequence 126, App	925	3	75.0	16	6	5443956-5	Patent No. 5443956
853	3	75.0	14	1	US-08-759-309A-6	Sequence 6, Appl	926	3	75.0	16	6	5443956-6	Patent No. 5443956
854	3	75.0	14	1	US-08-469-526A-126	Sequence 126, App	927	3	75.0	17	1	US-07-895-252-1	Sequence 1, Appl
855	3	75.0	14	2	US-08-734-591A-126	Sequence 126, App	928	3	75.0	17	1	US-08-072-283B-1	Sequence 1, Appl
856	3	75.0	14	2	US-08-469-560-126	Sequence 126, App	929	3	75.0	17	1	US-08-336-618-5	Sequence 5, Appl
857	3	75.0	14	2	US-08-685-589A-166	Sequence 166, App	930	3	75.0	17	2	US-08-986-234-36	Sequence 36, Appl
858	3	75.0	14	3	US-08-994-570-6	Sequence 6, Appl	931	3	75.0	17	3	US-08-782-997A-11	Sequence 11, Appl
859	3	75.0	14	4	US-08-470-335-126	Sequence 126, App	932	3	75.0	17	4	US-09-102-451-2	Sequence 2, Appl
860	3	75.0	14	4	US-08-735-021-126	Sequence 126, App	933	3	75.0	17	4	US-08-860-904-11	Sequence 11, Appl
861	3	75.0	14	4	US-08-734-664A-126	Sequence 126, App	934	3	75.0	17	4	US-08-860-904-18	Sequence 18, Appl
862	3	75.0	14	4	US-08-470-339-126	Sequence 126, App	935	3	75.0	17	4	US-08-860-904-19	Sequence 19, Appl
863	3	75.0	14	4	US-08-687-590-41	Sequence 41, Appl	936	3	75.0	17	4	US-08-860-904-20	Sequence 20, Appl
864	3	75.0	14	4	US-08-458-818B-13	Sequence 13, Appl	937	3	75.0	17	4	US-08-255-208A-50	Sequence 50, Appl
865	3	75.0	14	4	US-09-302-305C-12	Sequence 2, Appl	938	3	75.0	17	4	US-09-292-225-10	Sequence 10, Appl
866	3	75.0	14	4	US-08-302-305C-15	Sequence 15, Appl	939	3	75.0	17	4	US-09-082-335B-103	Sequence 103, App
867	3	75.0	14	4	US-08-949-059A-24	Sequence 24, Appl	940	3	75.0	18	1	US-07-798-776-7	Sequence 7, Appl
868	3	75.0	14	4	US-09-053-611-14	Sequence 14, Appl	941	3	75.0	18	1	US-08-076-092-2	Sequence 2, Appl
869	3	75.0	14	4	US-08-255-208A-47	Sequence 47, Appl	942	3	75.0	18	1	US-08-076-092-12	Sequence 12, Appl
870	3	75.0	14	4	US-08-467-602-126	Sequence 126, App	943	3	75.0	18	1	US-08-076-092-13	Sequence 13, Appl
871	3	75.0	14	5	PCT-US93-06171-31	Sequence 31, Appl	944	3	75.0	18	1	US-08-331-398A-55	Sequence 55, Appl
872	3	75.0	14	5	PCT-US94-05083C-142	Sequence 142, App	945	3	75.0	18	1	US-08-401-908-14	Sequence 14, Appl
873	3	75.0	14	5	PCT-US95-04075-31	Sequence 31, Appl	946	3	75.0	18	2	US-08-374-652C-90	Sequence 90, Appl
874	3	75.0	14	5	PCT-US95-06846A-126	Sequence 126, App	947	3	75.0	18	2	US-08-374-652C-92	Sequence 92, Appl
875	3	75.0	15	1	US-08-331-398A-66	Sequence 66, Appl	948	3	75.0	18	2	US-08-730-486-2	Sequence 2, Appl
876	3	75.0	15	1	US-08-208-181A-12	Sequence 12, Appl	949	3	75.0	18	2	US-08-730-486-12	Sequence 12, Appl
877	3	75.0	15	1	US-08-615-279-8	Sequence 8, Appl	950	3	75.0	18	2	US-08-730-486-13	Sequence 13, Appl
878	3	75.0	15	1	US-08-615-279-29	Sequence 29, Appl	951	3	75.0	18	2	US-08-331-397B-55	Sequence 55, Appl
879	3	75.0	15	2	US-08-642-684-9	Sequence 9, Appl	952	3	75.0	18	2	US-08-759-804A-54	Sequence 54, Appl
880	3	75.0	15	2	US-08-432-871C-72	Sequence 72, Appl	953	3	75.0	18	3	US-08-817-926-10	Sequence 10, Appl
881	3	75.0	15	2	US-08-960-128-6	Sequence 6, Appl	954	3	75.0	18	3	US-08-251-288A-7	Sequence 7, Appl
882	3	75.0	15	2	US-09-049-577-4	Sequence 4, Appl	955	3	75.0	18	3	US-09-276-202-7	Sequence 7, Appl
883	3	75.0	15	2	US-08-331-397B-66	Sequence 66, Appl	956	3	75.0	18	3	US-09-298-819A-7	Sequence 7, Appl
884	3	75.0	15	2	US-08-759-804A-65	Sequence 65, Appl	957	3	75.0	18	4	US-09-025-596-99	Sequence 99, Appl
885	3	75.0	15	2	US-08-553-257A-63	Sequence 63, Appl	958	3	75.0	18	4	US-08-255-208A-51	Sequence 51, Appl
886	3	75.0	15	2	US-08-569-147-39	Sequence 39, Appl	959	3	75.0	18	4	US-09-268-480-30	Sequence 30, Appl
887	3	75.0	15	4	US-09-001-984C-105	Sequence 105, App	960	3	75.0	19	1	US-07-977-696C-36	Sequence 36, Appl
888	3	75.0	15	4	US-09-390-598-4	Sequence 4, Appl	961	3	75.0	19	1	US-08-129-930B-35	Sequence 35, Appl
889	3	75.0	15	4	US-09-230-405-8	Sequence 8, Appl	962	3	75.0	19	2	US-08-672-610A-46	Sequence 46, Appl
890	3	75.0	15	4	US-08-630-347-4	Sequence 4, Appl	963	3	75.0	19	2	US-08-637-759B-254	Sequence 254, App
891	3	75.0	15	4	US-09-347-504-36	Sequence 36, Appl	964	3	75.0	19	2	US-08-584-671-5	Sequence 5, Appl
892	3	75.0	15	4	US-09-009-953-214	Sequence 214, App	965	3	75.0	19	2	US-08-706-741B-30	Sequence 30, Appl
893	3	75.0	15	4	US-08-255-208A-48	Sequence 48, App	966	3	75.0	19	2	US-08-924-695A-30	Sequence 30, Appl
894	3	75.0	15	4	US-09-270-956-72	Sequence 72, Appl	967	3	75.0	19	3	US-09-027-376-5	Sequence 5, Appl
895	3	75.0	15	4	US-08-766-586A-55	Sequence 55, Appl	968	3	75.0	19	3	US-08-871-355A-254	Sequence 254, App
896	3	75.0	15	4	US-08-766-586A-59	Sequence 59, Appl	969	3	75.0	19	3	US-08-792-832A-36	Sequence 36, Appl
897	3	75.0	15	6	5443956-1	Patent No. 5443956	970	3	75.0	19	4	US-09-094-192-5	Sequence 49, Appl
898	3	75.0	15	6	5470718-8	Patent No. 5470718	971	3	75.0	19	4	US-09-385-442-49	Sequence 49, Appl
899	3	75.0	16	1	US-08-279-058B-16	Sequence 16, Appl	972	3	75.0	19	4	US-09-385-442-50	Sequence 50, Appl
900	3	75.0	16	1	US-08-482-142-185	Sequence 185, App	973	3	75.0	19	4	US-08-134-346A-23	Sequence 23, Appl
901	3	75.0	16	2	US-08-482-142-186	Sequence 186, App	974	3	75.0	19	4	US-08-976-288A-36	Sequence 36, Appl
902	3	75.0	16	2	US-08-797-366-4	Sequence 4, Appl	975	3	75.0	19	4	US-09-201-945-254	Sequence 254, App
903	3	75.0	16	2	US-08-874-347-4	Sequence 4, Appl	976	3	75.0	19	4	US-09-171-156A-87	Sequence 87, Appl

977 3 75.0 19 4 US-08-255-208A-52 Sequence 52, Appl  
978 3 75.0 20 2 US-08-319-376-4 Sequence 4, Appl  
979 3 75.0 20 2 US-08-481-658B-52 Sequence 52, Appl  
980 3 75.0 20 2 US-08-031-538-61 Sequence 61, Appl  
981 3 75.0 20 2 US-08-031-538-66 Sequence 66, Appl  
982 3 75.0 20 2 US-08-477-504A-52 Sequence 52, Appl  
983 3 75.0 20 2 US-08-955-138-94 Sequence 94, Appl  
984 3 75.0 20 2 US-08-486-756A-52 Sequence 52, Appl  
985 3 75.0 20 2 US-08-485-862B-52 Sequence 52, Appl  
986 3 75.0 20 3 US-08-787-739-52 Sequence 52, Appl  
987 3 75.0 20 3 US-08-448-194-14 Sequence 14, Appl  
988 3 75.0 20 3 US-08-487-077A-52 Sequence 52, Appl  
989 3 75.0 20 3 US-08-485-863A-52 Sequence 52, Appl  
990 3 75.0 20 4 US-08-485-049D-52 Sequence 52, Appl  
991 3 75.0 20 4 US-09-178-115-52 Sequence 52, Appl  
992 3 75.0 20 4 US-09-177-776-52 Sequence 14, Appl  
993 3 75.0 20 4 US-08-867-921-14 Sequence 14, Appl  
994 3 75.0 20 4 US-09-439-313-567 Sequence 567, App  
995 3 75.0 20 4 US-09-230-405-7 Sequence 7, Appl  
996 3 75.0 20 4 US-09-556-877-245 Sequence 245, App  
997 3 75.0 20 4 US-09-556-877-246 Sequence 246, App  
998 3 75.0 20 4 US-09-556-877-247 Sequence 247, App  
999 3 75.0 20 4 US-08-255-208A-53 Sequence 53, Appl  
1000 3 75.0 20 4 US-09-620-412C-245 Sequence 245, App

## ALIGNMENTS

RESULT 1  
US-08-970-833-1  
; Sequence 1, Application US/08970833  
; Patent No. 6022859  
; GENERAL INFORMATION:  
; APPLICANT: Kieselring, Laura L.  
; APPLICANT: Murphy, Regina M.  
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/970,833  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 960296.94291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 271-5709  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-970-833-1

Query Match 100.0%; Score 4; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 2  
US-08-664-379B-17  
; Sequence 17, Application US/08664379B  
; Patent No. 6034211  
; GENERAL INFORMATION:  
; APPLICANT: Kelly, Jeffery W.  
; TITLE OF INVENTION: BETA-SHEET NUCLEATING PEPTIDOMIMETICS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/664,379B  
; FILING DATE: 14-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/018,925  
; FILING DATE: 03-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 08435/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-664-379B-17

Query Match 100.0%; Score 4; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 3  
US-09-095-106A-25  
; Sequence 25, Application US/09095106A  
; Patent No. 6331440  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: THYBERG, Johan  
; APPLICANT: TJERNBERG, Lars O.  
; APPLICANT: TERENIUS, Lars  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 000500-124  
; CURRENT APPLICATION NUMBER: US/09/095,106A  
; CURRENT FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29

PRIOR APPLICATION NUMBER: PCT/SE96/01621  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 25  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Amyloidosis  
US-09-095-106A-25

Query Match 100.0%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 4  
US-08-127-904-15  
Sequence 15, Application US/08127904  
Patent No. 5470951

GENERAL INFORMATION:  
APPLICANT: Eugene Roberts  
TITLE OF INVENTION: Method For Antagonizing  
TITLE OF INVENTION: Amnestic Effects of Amyloid n  
TITLE OF INVENTION: Protein and Improving the  
TITLE OF INVENTION: Quality of Life in Individuals  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: City of Hope  
STREET: 1500 East Duarte Road  
City: Duarte  
STATE: California  
COUNTRY: United States of America  
ZIP: 91010-0269  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3M Double Density 5 1/4" diskette  
COMPUTER: Wang PC  
OPERATING SYSTEM: MS DOS Version 3.20  
SOFTWARE: Microsoft  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,904  
FILING DATE: 29 September 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA: No. 5470951e  
ATTORNEY/AGENT INFORMATION:  
NAME: Irons, Edward S.  
REGISTRATION NUMBER: 16,541  
REFERENCE/DOCKET NUMBER: No. 5470951e  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Unknown  
US-08-127-904-15

Query Match 100.0%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 5  
US-08-612-785B-10  
Sequence 10, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHYE & COCKFIELD  
STREET: 28 State Street, Suite 510  
City: Boston  
STATE: Massachusetts  
COUNTRY: USA

ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConci, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-10

Query Match 100.0%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 6  
US-08-970-833-2  
Sequence 2, Application US/08970833  
Patent No. 6022859  
GENERAL INFORMATION:  
APPLICANT: Kieselring, Laura L.  
APPLICANT: Murphy, Regina M.  
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 411 East Wisconsin Avenue  
City: Milwaukee  
STATE: Wisconsin  
COUNTRY: U.S.A.

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; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-970-833-2

Query Match 100.0%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   ||||
Db 1 KLVF 4

RESULT 7
US-08-703-675C-46
; Sequence 46, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
```

```
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-46

Query Match 100.0%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   ||||
Db 1 KLVF 4

RESULT 8
US-09-242-724-25
; Sequence 25, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; APPLICANT: Rich, Daniel H.
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
; FILE REFERENCE: Cyclosporin Analogs
; CURRENT APPLICATION NUMBER: US/09/242,724
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-09-242-724-25

Query Match 100.0%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   ||||
Db 1 KLVF 4

RESULT 9
US-09-242-724-26
; Sequence 26, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; APPLICANT: Rich, Daniel H.
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
; FILE REFERENCE: Cyclosporin Analogs
; CURRENT APPLICATION NUMBER: US/09/242,724
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: ACETYLTATION; K(2Cl-Cbz) =
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OTHER INFORMATION: 2-chlorobenzoyloxycarbonyl-protected lysine  
US-09-242-724-26

Query Match 100.0%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 10  
US-08-617-267C-10  
Sequence 10, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02109-1875  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Decont, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPT-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-10

Query Match 100.0%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 11  
US-08-617-267C-37  
Sequence 37, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:

APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02109-1875  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Decont, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPT-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-617-267C-37

Query Match 100.0%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 2 KLVF 5

RESULT 12  
US-09-095-106A-1  
Sequence 1, Application US/09095106A  
Patent No. 6331440  
GENERAL INFORMATION:  
APPLICANT: NORDSTEDT, Christer  
APPLICANT: NASLUND, Jan  
APPLICANT: THYBERG, Johan  
APPLICANT: TERNERUS, Lars O.  
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
FILE REFERENCE: 000500-124  
CURRENT APPLICATION NUMBER: US/09/095,106A  
CURRENT FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: US 60/009,386  
PRIOR FILING DATE: 1995-12-29  
PRIOR APPLICATION NUMBER: PCT/SE96/01621  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1

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; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-1

Query Match      100.0%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 13
US-09-095-106A-19
; Sequence 19, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TUERNBERG, Lars O.
; APPLICANT: TERNIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-19

Query Match      100.0%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 2 KLVF 5

RESULT 14
US-09-095-106A-43
; Sequence 43, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TUERNBERG, Lars O.
; APPLICANT: TERNIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-43

Query Match      100.0%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 15
US-09-095-106A-43
; Sequence 15, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Anesthetic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
PCT-US94-10475-15

Query Match      100.0%; Score 4; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 16
US-08-612-785B-8
; Sequence 8, Application US/08612785B
```



```
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Deconci, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-612-785B-8

Query Match          100.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVF 4
        ||||
Db      2 KLVF 5

RESULT 17
; US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Deconci, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-612-785B-9

Query Match          100.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVF 4
        ||||
Db      1 KLVF 4

RESULT 18
; US-08-612-785B-31
; Sequence 31, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
```

```
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
;
US-08-612-785B-31

Query Match 100.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 1 KLVF 4

RESULT 19
US-08-664-379B-19
; Sequence 19, Application US/08664379B
; Patent No. 6034211
; GENERAL INFORMATION:
; APPLICANT: Kelly, Jeffery W.
; TITLE OF INVENTION: BETA-SHEET NUCLEATING PEPTIDOMIMETICS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,379B
; FILING DATE: 14-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,925
; FILING DATE: 03-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 08435/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; LOCATION: 1...1
; OTHER INFORMATION: wherein Xaa at position 1 is Ornithine
;
US-08-664-379B-19
```

```
Query Match 100.0%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 2 KLVF 5

RESULT 20
US-08-703-675C-31
; Sequence 31, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-703-675C-31

Query Match 100.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 2 KLVF 5

RESULT 21
US-08-703-675C-32
; Sequence 32, Application US/08703675C
```

```

; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findex, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-32

Query Match          100.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 22
US-08-703-675C-44
; Sequence 44, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findex, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note=Xaa is beta-alanyl
; US-08-703-675C-44

Query Match          100.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 1 KLVF 4

RESULT 23
US-09-242-724-24
; Sequence 24, Application US/09242724
; Patent No. 6316405
; GENERAL INFORMATION:
; APPLICANT: Solomon, Michael E.
; APPLICANT: Rich, Daniel H.
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
; FILE REFERENCE: Cyclosporin Analogs
; CURRENT APPLICATION NUMBER: US/09/242,724
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-09-242-724-24

Query Match          100.0%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 KLVF 4  
Db 2 KLVF 5

## RESULT 24

US-09-242-724-27  
; Sequence 27, Application US/09242724  
; Patent No. 6316405  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, Michael E.  
; APPLICANT: Rich, Daniel H.  
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor  
; FILE REFERENCE: Cyclosporin Analogs  
; CURRENT APPLICATION NUMBER: US/09/242,724  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; NAME/KEY: MOD RES  
; LOCATION: (1)  
; OTHER INFORMATION: ACETYLATION  
; NAME/KEY: MOD RES  
; LOCATION: (2)  
; OTHER INFORMATION: K(2Cl-Cbz) = 2-chlorobenzylloxycarbonyl-protected  
; OTHER INFORMATION: lysine  
; US-09-242-724-27

Query Match 100.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 2 KLVF 5

## RESULT 25

US-09-242-724-30  
; Sequence 30, Application US/09242724  
; Patent No. 6316405  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, Michael E.  
; APPLICANT: Rich, Daniel H.  
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor  
; FILE REFERENCE: Cyclosporin Analogs  
; CURRENT APPLICATION NUMBER: US/09/242,724  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; US-09-242-724-30

Query Match 100.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 2 KLVF 5

## RESULT 26

US-09-242-724-31  
; Sequence 31, Application US/09242724  
; Patent No. 6316405  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, Michael E.  
; APPLICANT: Rich, Daniel H.  
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor  
; FILE REFERENCE: Cyclosporin Analogs  
; CURRENT APPLICATION NUMBER: US/09/242,724  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide  
; US-09-242-724-31

Query Match 100.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

## RESULT 27

US-09-242-724-33  
; Sequence 33, Application US/09242724  
; Patent No. 6316405  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, Michael E.  
; APPLICANT: Rich, Daniel H.  
; TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor  
; FILE REFERENCE: Cyclosporin Analogs  
; CURRENT APPLICATION NUMBER: US/09/242,724  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide  
; US-09-242-724-33

Query Match 100.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 2 KLVF 5

## RESULT 28

US-08-617-267C-8  
; Sequence 8, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:  
; APPLICANT: Findels, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Decontli, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-8

Query Match 100.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 2 KLVF 5

RESULT 29  
US-08-617-267C-9  
Sequence 9, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Decontli, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-9

Query Match 100.0%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 30  
US-08-617-267C-31  
Sequence 31, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Decontli, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

```
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
US-08-617-267C-31

Query Match
Best Local Similarity 100.0%; Score 4; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 1 KLVF 4

RESULT 31
US-08-617-267C-43
; Sequence 43, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-43

Query Match
Best Local Similarity 100.0%; Score 4; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 2 KLVF 5
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RESULT 32
US-09-095-106A-5
; Sequence 5, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TUERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-5

Query Match
Best Local Similarity 100.0%; Score 4; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 2 KLVF 5

RESULT 33
US-09-095-106A-15
; Sequence 15, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TUERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-15

Query Match
Best Local Similarity 100.0%; Score 4; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 3 KLVF 6

RESULT 34
US-08-127-904-14
; Sequence 14, Application US/08127904
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Patent No. 5470951  
GENERAL INFORMATION:  
APPLICANT: Eugene Roberts  
TITLE OF INVENTION: Method For Antagonizing  
TITLE OF INVENTION: Amnesic Effects of Amyloid n  
TITLE OF INVENTION: Protein and Improving the  
TITLE OF INVENTION: Quality of Life in Individuals  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: City of Hope  
STREET: 1500 East Duarte Road  
CITY: Duarte  
STATE: California  
COUNTRY: United States of America  
ZIP: 91010-0269  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3M Double Density 5 1/4" diskette  
COMPUTER: Wang PC  
OPERATING SYSTEM: MS DOS Version 3.20  
SOFTWARE: Microsoft  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,904  
FILING DATE: 29 September 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
ATTORNEY/AGENT INFORMATION:  
NAME: Irons, Edward S.  
REGISTRATION NUMBER: 16,541  
REFERENCE/DOCKET NUMBER: No. 5470951e  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
TELEX: No. 5470951e  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Unknown  
US-08-127-904-14

Query Match 100.0%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 35  
US-08-612-785B-6  
Sequence 6, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findels, Mark A. et al.  
TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-6

Query Match 100.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 3 KLVF 6

RESULT 36  
US-08-612-785B-7  
Sequence 7, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findels, Mark A. et al.  
TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-612-785B-7

Query Match 100.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 KLVF 4  
|||  
Db 2 KLVF 5

RESULT 37  
US-08-703-675C-29  
; Sequence 29, Application US/08703675C  
; Patent No. 6303567  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/703,675C  
; FILING DATE: 27-AUG-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-016CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-703-675C-29

Query Match 100.0%; Score 4; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 3 KLVF 6

RESULT 38  
US-08-703-675C-30  
; Sequence 30, Application US/08703675C  
; Patent No. 6303567  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/703,675C  
; FILING DATE: 27-AUG-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-016CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-703-675C-30

Query Match 100.0%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 2 KLVF 5

RESULT 39  
US-08-617-267C-6  
; Sequence 6, Application US/08617267C  
; Patent No. 6319498  
; GENERAL INFORMATION:



APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C  
FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-6  
Query Match 100.0%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
DB 3 KLVF 6  
RESULT 40  
US-08-617-267C-7  
Sequence 7, Application US/08617267C  
Patent No. 6319498  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Modulators of Amyloid Aggregation  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,267C

FILING DATE: 14-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-617-267C-7

Query Match 100.0%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVF 4  
DB 2 KLVF 5

Search completed: January 3, 2003, 07:59:57  
Job time: 29 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:53:12 ; Search time 11 Seconds  
(without alignments)  
6.891 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 4

Sequence: 1 KLVF 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 117078 seqs, 18951520 residues

Word size : 0

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Published Applications\_AA.\*  
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2: /cgn2\_6/prodata/1/pubppaa/PCT\_NEW\_PUB pep.\*  
3: /cgn2\_6/prodata/1/pubppaa/US06\_NEW\_PUB pep.\*  
4: /cgn2\_6/prodata/1/pubppaa/US06\_PUBCOMB pep.\*  
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14: /cgn2\_6/prodata/1/pubppaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	4	100.0	4	10	US-09-850-061A-25
4	4	100.0	5	10	US-09-867-847-17
5	4	100.0	5	10	US-09-867-847-25
6	4	100.0	5	10	US-09-850-061A-19
7	4	100.0	5	10	US-09-850-061A-11
8	4	100.0	5	10	US-09-850-061A-43
9	4	100.0	5	10	US-09-972-475-10
10	4	100.0	5	10	US-09-972-475-37
11	4	100.0	6	10	US-09-867-847-7
12	4	100.0	6	10	US-09-867-847-20
13	4	100.0	6	10	US-09-867-847-52
14	4	100.0	6	10	US-09-867-847-55
15	4	100.0	6	10	US-09-867-847-58
16	4	100.0	6	10	US-09-867-847-61
17	4	100.0	6	10	US-09-867-847-64
18	4	100.0	6	10	US-09-850-061A-5
19	4	100.0	6	10	US-09-850-061A-15

20	4	100.0	6	10	US-09-972-475-8	Sequence 8, Appli
21	4	100.0	6	10	US-09-972-475-9	Sequence 9, Appli
22	4	100.0	6	10	US-09-972-475-31	Sequence 31, Appli
23	4	100.0	6	10	US-09-972-475-43	Sequence 43, Appli
24	4	100.0	6	10	US-09-966-625-25	Sequence 25, Appli
25	4	100.0	7	10	US-09-867-847-12	Sequence 12, Appli
26	4	100.0	7	10	US-09-867-847-27	Sequence 27, Appli
27	4	100.0	7	10	US-09-867-847-28	Sequence 28, Appli
28	4	100.0	7	10	US-09-850-061A-11	Sequence 11, Appli
29	4	100.0	7	10	US-09-850-061A-12	Sequence 12, Appli
30	4	100.0	7	10	US-09-972-475-6	Sequence 6, Appli
31	4	100.0	7	10	US-09-972-475-7	Sequence 7, Appli
32	4	100.0	8	10	US-09-850-061A-8	Sequence 8, Appli
33	4	100.0	8	10	US-09-850-061A-9	Sequence 9, Appli
34	4	100.0	8	10	US-09-850-061A-44	Sequence 44, Appli
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94	4	100.0	53	10	US-09-797-543-5	Sequence 5, Appli	167	4	100.0	319	9	US-10-114-893-90	Sequence 90, Appli
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97	4	100.0	54	10	US-09-823-153-10	Sequence 10, Appli	170	4	100.0	344	10	US-09-912-025-2	Sequence 2, Appli
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101	4	100.0	60	12	US-10-060-506-21	Sequence 21, Appli	173	4	100.0	353	10	US-09-739-451-12	Sequence 12, Appli
102	4	100.0	61	10	US-09-867-550-1882	Sequence 1882, Ap	174	4	100.0	355	10	US-09-794-975-13	Sequence 13, Appli
103	4	100.0	65	10	US-09-764-869-999	Sequence 999, App	175	4	100.0	360	10	US-09-815-242-11598	Sequence 11598, A
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107	4	100.0	73	10	US-09-522-217-687	Sequence 687, App	179	4	100.0	364	12	US-10-112-357-4	Sequence 4, Appli
108	4	100.0	73	10	US-09-833-263-687	Sequence 687, App	180	4	100.0	364	12	US-10-114-403-4	Sequence 4, Appli
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115	4	100.0	97	9	US-09-895-913A-58	Sequence 58, Appli	187	4	100.0	366	12	US-10-060-509-2	Sequence 2, Appli
116	4	100.0	100	10	US-09-794-975-4	Sequence 4, Appli	188	4	100.0	366	12	US-10-060-506-2	Sequence 2, Appli
117	4	100.0	101	10	US-09-799-118-6	Sequence 6, Appli	189	4	100.0	366	12	US-10-060-506-4	Sequence 4, Appli
118	4	100.0	103	10	US-09-972-475-2	Sequence 2, Appli	190	4	100.0	378	12	US-10-021-758-2	Sequence 2, Appli
119	4	100.0	103	10	US-09-895-443-2	Sequence 2, Appli	191	4	100.0	383	9	US-09-895-913A-152	Sequence 152, App
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121	4	100.0	117	10	US-09-794-975-6	Sequence 6, Appli	193	4	100.0	412	12	US-10-090-624-1	Sequence 1, Appli
122	4	100.0	117	10	US-09-823-153-2	Sequence 2, Appli	194	4	100.0	417	10	US-09-815-242-10592	Sequence 10592, A
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124	4	100.0	133	10	US-09-738-769A-4	Sequence 4, Appli	196	4	100.0	424	9	US-09-989-293A-14	Sequence 14, Appli
125	4	100.0	140	10	US-09-815-242-13616	Sequence 13616, A	197	4	100.0	424	9	US-09-989-733-14	Sequence 14, Appli
126	4	100.0	140	10	US-09-932-702-2	Sequence 2, Appli	198	4	100.0	424	9	US-09-990-444-14	Sequence 14, Appli
127	4	100.0	144	10	US-09-939-980-445	Sequence 445, App	199	4	100.0	424	9	US-09-989-730-14	Sequence 14, Appli
128	4	100.0	148	12	US-10-052-586-456	Sequence 456, App	200	4	100.0	424	9	US-09-990-436-14	Sequence 14, Appli
129	4	100.0	149	10	US-09-925-301-882	Sequence 882, App	201	4	100.0	424	9	US-09-991-181-14	Sequence 14, Appli
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131	4	100.0	162	9	US-09-989-920-199	Sequence 199, App	203	4	100.0	424	10	US-09-989-722-14	Sequence 14, Appli
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137	4	100.0	208	9	US-10-08-605-45	Sequence 45, Appli	209	4	100.0	424	10	US-09-991-073-14	Sequence 14, Appli
138	4	100.0	209	10	US-09-811-284-225	Sequence 225, App	210	4	100.0	424	10	US-09-990-442-14	Sequence 14, Appli
139	4	100.0	217	10	US-09-925-300-1364	Sequence 1364, Ap	211	4	100.0	424	10	US-09-991-163-14	Sequence 14, Appli
140	4	100.0	219	10	US-09-764-864-946	Sequence 946, App	212	4	100.0	424	10	US-09-993-604-14	Sequence 14, Appli
141	4	100.0	227	10	US-09-030-847-5	Sequence 5, Appli	213	4	100.0	424	10	US-09-990-456-14	Sequence 14, Appli
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143	4	100.0	227	12	US-10-039-865-5	Sequence 5, Appli	215	4	100.0	424	12	US-10-052-586-8	Sequence 8, Appli
144	4	100.0	228	1	US-09-976-063C-14	Sequence 14, Appli	216	4	100.0	429	10	US-09-922-501-10	Sequence 10, Appli
145	4	100.0	247	10	US-09-996-357-13	Sequence 13, Appli	217	4	100.0	431	8	US-08-981-087A-1	Sequence 1, Appli
146	4	100.0	254	10	US-09-912-787-12	Sequence 12, Appli	218	4	100.0	448	12	US-10-029-756-5	Sequence 5, Appli
147	4	100.0	254	10	US-09-912-787-71	Sequence 71, Appli	219	4	100.0	450	10	US-09-815-242-13434	Sequence 13434, A
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150	4	100.0	255	10	US-09-897-214-2	Sequence 2, Appli	222	4	100.0	479	10	US-09-952-768-2	Sequence 2, Appli
151	4	100.0	255	10	US-09-893-737-232	Sequence 232, App	223	4	100.0	479	10	US-09-410-194-20	Sequence 20, Appli
152	4	100.0	256	10	US-09-815-242-5228	Sequence 5228, Ap	224	4	100.0	479	10	US-09-954-697-33	Sequence 33, Appli
153	4	100.0	256	10	US-09-815-242-12535	Sequence 12535, A	225	4	100.0	479	10	US-09-888-243-6	Sequence 6, Appli
154	4	100.0	256	10	US-09-815-242-12892	Sequence 12892, A	226	4	100.0	496	9	US-09-738-626-4925	Sequence 4925, Ap
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156	4	100.0	270	10	US-09-765-272-64	Sequence 64, Appli	228	4	100.0	505	10	US-09-888-243-5	Sequence 5, Appli
157	4	100.0	275	9	US-09-854-133-584	Sequence 584, App	229	4	100.0	513	9	US-09-738-626-3645	Sequence 3645, Ap
158	4	100.0	275	10	US-09-738-973-584	Sequence 584, App	230	4	100.0	522	12	US-10-090-624-4	Sequence 4, Appli
159	4	100.0	279	10	US-09-764-870-539	Sequence 539, App	231	4	100.0	566	10	US-09-829-482-5	Sequence 5, Appli
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161	4	100.0	286	10	US-09-862-915-1	Sequence 1, Appli	233	4	100.0	573	10	US-09-815-242-11257	Sequence 11257, A
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163	4	100.0	301	9	US-10-080-960-11	Sequence 11, Appli	235	4	100.0	618	10	US-09-995-007-2	Sequence 2, Appli
164	4	100.0	302	10	US-09-948-078-2	Sequence 2, Appli	236	4	100.0	654	12	US-10-090-624-16	Sequence 16, Appli
165	4	100.0	308	10	US-09-764-870-433	Sequence 433, App	237	4	100.0	657	10	US-09-866-866A-14	Sequence 14, Appli
	4	100.0	308	10	US-09-764-870-538	Sequence 538, App	238	4	100.0	669	9	US-09-983-204-15	Sequence 15, Appli

239	4	100.0	669	9	US-10-133-157-4	Sequence 4, Appl	312	4	100.0	867	10	US-09-815-242-10654	Sequence 10654, A
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244	4	100.0	695	10	US-09-794-927-12	Sequence 12, Appl	317	4	100.0	933	10	US-09-815-242-11817	Sequence 11817, A
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247	4	100.0	695	10	US-09-795-847-11	Sequence 11, Appl	320	4	100.0	1111	9	US-09-738-626-6581	Sequence 6581, Ap
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249	4	100.0	695	10	US-09-794-743-10	Sequence 10, Appl	322	4	100.0	1140	9	US-10-108-605-292	Sequence 293, App
250	4	100.0	695	10	US-09-794-743-12	Sequence 12, Appl	323	4	100.0	2026	10	US-09-801-368-86	Sequence 86, Appl
251	4	100.0	695	10	US-09-794-743-14	Sequence 14, Appl	324	4	100.0	3092	10	US-09-801-368-172	Sequence 172, App
252	4	100.0	695	10	US-09-794-748-10	Sequence 10, Appl	325	3	75.0	3	10	US-09-850-061A-32	Sequence 32, Appl
253	4	100.0	695	10	US-09-794-748-12	Sequence 12, Appl	326	3	75.0	3	10	US-09-850-061A-33	Sequence 33, Appl
254	4	100.0	695	10	US-09-794-748-14	Sequence 14, Appl	327	3	75.0	3	10	US-09-895-443-10	Sequence 10, Appl
255	4	100.0	695	10	US-09-794-925-10	Sequence 10, Appl	328	3	75.0	4	8	US-08-450-842-92	Sequence 92, Appl
256	4	100.0	695	10	US-09-794-925-12	Sequence 12, Appl	329	3	75.0	4	8	US-08-484-409-19	Sequence 19, Appl
257	4	100.0	695	10	US-09-794-925-14	Sequence 14, Appl	330	3	75.0	4	10	US-09-850-061A-24	Sequence 24, Appl
258	4	100.0	695	10	US-09-681-442-10	Sequence 10, Appl	331	3	75.0	4	10	US-09-850-061A-26	Sequence 26, Appl
259	4	100.0	695	10	US-09-681-442-12	Sequence 12, Appl	332	3	75.0	4	10	US-09-972-475-12	Sequence 12, Appl
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261	4	100.0	695	10	US-09-149-718-2	Sequence 2, Appl	334	3	75.0	4	10	US-09-895-443-9	Sequence 9, Appl
262	4	100.0	697	10	US-09-794-927-16	Sequence 16, Appl	335	3	75.0	4	10	US-09-895-443-13	Sequence 13, Appl
263	4	100.0	697	10	US-09-794-927-18	Sequence 18, Appl	336	3	75.0	4	10	US-09-895-443-14	Sequence 14, Appl
264	4	100.0	697	10	US-09-794-927-20	Sequence 20, Appl	337	3	75.0	4	10	US-09-895-443-15	Sequence 15, Appl
265	4	100.0	697	10	US-09-795-847-16	Sequence 16, Appl	338	3	75.0	4	10	US-09-996-357-2	Sequence 2, Appl
266	4	100.0	697	10	US-09-795-847-18	Sequence 18, Appl	339	3	75.0	4	10	US-09-781-133-1	Sequence 1, Appl
267	4	100.0	697	10	US-09-795-847-20	Sequence 20, Appl	340	3	75.0	4	10	US-09-781-133-3	Sequence 3, Appl
268	4	100.0	697	10	US-09-794-743-16	Sequence 16, Appl	341	3	75.0	4	10	US-09-781-133-6	Sequence 6, Appl
269	4	100.0	697	10	US-09-794-743-18	Sequence 18, Appl	342	3	75.0	4	10	US-09-781-133-7	Sequence 7, Appl
270	4	100.0	697	10	US-09-794-743-20	Sequence 20, Appl	343	3	75.0	4	10	US-09-781-133-8	Sequence 8, Appl
271	4	100.0	697	10	US-09-794-748-16	Sequence 16, Appl	344	3	75.0	5	10	US-09-867-847-45	Sequence 45, Appl
272	4	100.0	697	10	US-09-794-748-18	Sequence 18, Appl	345	3	75.0	5	10	US-09-867-847-46	Sequence 46, Appl
273	4	100.0	697	10	US-09-794-748-20	Sequence 20, Appl	346	3	75.0	5	10	US-09-867-847-47	Sequence 47, Appl
274	4	100.0	697	10	US-09-794-925-16	Sequence 16, Appl	347	3	75.0	5	10	US-09-867-847-48	Sequence 48, Appl
275	4	100.0	697	10	US-09-794-925-18	Sequence 18, Appl	348	3	75.0	5	10	US-09-867-847-49	Sequence 49, Appl
276	4	100.0	697	10	US-09-794-925-20	Sequence 20, Appl	349	3	75.0	5	10	US-09-867-847-50	Sequence 50, Appl
277	4	100.0	697	10	US-09-681-442-16	Sequence 16, Appl	350	3	75.0	5	10	US-09-850-061A-20	Sequence 20, Appl
278	4	100.0	697	10	US-09-681-442-18	Sequence 18, Appl	351	3	75.0	5	10	US-09-850-061A-39	Sequence 39, Appl
279	4	100.0	697	10	US-09-681-442-20	Sequence 20, Appl	352	3	75.0	5	10	US-09-850-061A-42	Sequence 42, Appl
280	4	100.0	705	9	US-09-808-602-94	Sequence 94, Appl	353	3	75.0	5	10	US-09-972-475-11	Sequence 11, Appl
281	4	100.0	708	9	US-09-738-626-5024	Sequence 5024, Ap	354	3	75.0	5	10	US-09-972-475-22	Sequence 22, Appl
282	4	100.0	714	10	US-09-768-877-22	Sequence 22, Appl	355	3	75.0	5	10	US-09-972-475-26	Sequence 26, Appl
283	4	100.0	751	10	US-09-794-927-57	Sequence 57, Appl	356	3	75.0	5	10	US-09-972-475-30	Sequence 30, Appl
284	4	100.0	751	10	US-09-795-847-57	Sequence 57, Appl	357	3	75.0	5	10	US-09-972-475-32	Sequence 32, Appl
285	4	100.0	751	10	US-09-794-743-57	Sequence 57, Appl	358	3	75.0	5	10	US-09-972-475-41	Sequence 41, Appl
286	4	100.0	751	10	US-09-794-748-57	Sequence 57, Appl	359	3	75.0	5	10	US-09-895-443-3	Sequence 3, Appl
287	4	100.0	751	10	US-09-794-925-57	Sequence 57, Appl	360	3	75.0	5	10	US-09-895-443-16	Sequence 16, Appl
288	4	100.0	751	10	US-09-681-442-57	Sequence 57, Appl	361	3	75.0	5	10	US-09-895-443-20	Sequence 20, Appl
289	4	100.0	751	10	US-09-149-718-4	Sequence 4, Appl	362	3	75.0	5	10	US-09-895-443-21	Sequence 21, Appl
290	4	100.0	753	10	US-09-794-927-61	Sequence 61, Appl	363	3	75.0	5	10	US-09-895-443-27	Sequence 27, Appl
291	4	100.0	753	10	US-09-795-847-61	Sequence 61, Appl	364	3	75.0	5	10	US-09-895-443-28	Sequence 28, Appl
292	4	100.0	753	10	US-09-794-743-61	Sequence 61, Appl	365	3	75.0	5	10	US-09-895-443-33	Sequence 33, Appl
293	4	100.0	753	10	US-09-794-748-61	Sequence 61, Appl	366	3	75.0	5	10	US-09-895-443-34	Sequence 34, Appl
294	4	100.0	753	10	US-09-794-925-61	Sequence 61, Appl	367	3	75.0	5	10	US-09-996-357-3	Sequence 3, Appl
295	4	100.0	753	10	US-09-681-442-61	Sequence 61, Appl	368	3	75.0	5	10	US-09-781-133-2	Sequence 2, Appl
296	4	100.0	758	10	US-09-735-101-2	Sequence 2, Appl	369	3	75.0	5	10	US-09-781-133-12	Sequence 12, Appl
297	4	100.0	770	9	US-09-785-215-2	Sequence 2, Appl	370	3	75.0	5	10	US-09-781-133-13	Sequence 13, Appl
298	4	100.0	770	10	US-09-794-927-55	Sequence 55, Appl	371	3	75.0	6	9	US-09-935-194-8	Sequence 8, Appl
299	4	100.0	770	10	US-09-795-847-55	Sequence 55, Appl	372	3	75.0	6	10	US-09-867-847-51	Sequence 51, Appl
300	4	100.0	770	10	US-09-794-743-55	Sequence 55, Appl	373	3	75.0	6	10	US-09-867-847-53	Sequence 53, Appl
301	4	100.0	770	10	US-09-794-748-55	Sequence 55, Appl	374	3	75.0	6	10	US-09-867-847-54	Sequence 54, Appl
302	4	100.0	770	10	US-09-904-987-2	Sequence 2, Appl	375	3	75.0	6	10	US-09-867-847-56	Sequence 56, Appl
303	4	100.0	770	10	US-09-794-925-55	Sequence 55, Appl	376	3	75.0	6	10	US-09-867-847-57	Sequence 57, Appl
304	4	100.0	770	10	US-09-681-442-55	Sequence 55, Appl	377	3	75.0	6	10	US-09-867-847-59	Sequence 59, Appl
305	4	100.0	772	10	US-09-149-718-6	Sequence 6, Appl	378	3	75.0	6	10	US-09-867-847-60	Sequence 60, Appl
306	4	100.0	772	10	US-09-794-927-59	Sequence 59, Appl	379	3	75.0	6	10	US-09-867-847-62	Sequence 62, Appl
307	4	100.0	772	10	US-09-795-847-59	Sequence 59, Appl	380	3	75.0	6	10	US-09-867-847-63	Sequence 63, Appl
308	4	100.0	772	10	US-09-794-743-59	Sequence 59, Appl	381	3	75.0	6	10	US-09-867-847-65	Sequence 65, Appl
309	4	100.0	772	10	US-09-794-748-59	Sequence 59, Appl	382	3	75.0	6	10	US-09-850-061A-16	Sequence 16, Appl
310	4	100.0	772	10	US-09-794-925-59	Sequence 59, Appl	383	3	75.0	6	10	US-09-972-475-27	Sequence 27, Appl
311	4	100.0	772	10	US-09-681-442-59	Sequence 59, Appl	384	3	75.0	7	10	US-09-850-061A-13	Sequence 13, Appl

385	3	75.0	8	10	US-09-785-474-20	Sequence 20, Appl	458	3	75.0	18	10	US-09-734-520-1	Sequence 1, Appl
386	3	75.0	8	10	US-09-850-061A-10	Sequence 10, Appl	459	3	75.0	18	10	US-09-734-520-2	Sequence 2, Appl
387	3	75.0	9	1	US-08-821-739A-72	Sequence 72, Appl	460	3	75.0	18	10	US-09-734-520-3	Sequence 3, Appl
388	3	75.0	9	8	US-08-812-393A-64	Sequence 64, Appl	461	3	75.0	18	10	US-09-734-520-4	Sequence 4, Appl
389	3	75.0	9	9	US-09-824-787B-97	Sequence 97, Appl	462	3	75.0	18	10	US-09-734-520-5	Sequence 5, Appl
390	3	75.0	9	9	US-09-824-787B-99	Sequence 99, Appl	463	3	75.0	18	10	US-09-734-520-6	Sequence 6, Appl
391	3	75.0	9	9	US-09-824-787B-132	Sequence 132, Appl	464	3	75.0	18	10	US-09-734-520-45	Sequence 45, Appl
392	3	75.0	9	9	US-10-205-150-9	Sequence 9, Appl	465	3	75.0	18	12	US-10-012-034A-1	Sequence 1, Appl
393	3	75.0	9	9	US-09-826-177-52	Sequence 52, Appl	466	3	75.0	18	12	US-10-012-034A-2	Sequence 2, Appl
394	3	75.0	9	10	US-09-826-177-54	Sequence 54, Appl	467	3	75.0	18	12	US-10-012-034A-3	Sequence 3, Appl
395	3	75.0	9	10	US-09-898-461-5	Sequence 5, Appl	468	3	75.0	18	12	US-10-012-034A-4	Sequence 4, Appl
396	3	75.0	9	10	US-09-780-053-120	Sequence 120, App	469	3	75.0	18	12	US-10-012-034A-5	Sequence 5, Appl
397	3	75.0	9	10	US-09-780-053-563	Sequence 563, App	470	3	75.0	18	12	US-10-012-034A-6	Sequence 6, Appl
398	3	75.0	9	10	US-09-780-053-652	Sequence 652, App	471	3	75.0	18	12	US-10-012-034A-45	Sequence 45, Appl
399	3	75.0	9	10	US-09-894-018-146	Sequence 146, App	472	3	75.0	18	12	US-10-012-030A-81	Sequence 81, Appl
400	3	75.0	9	10	US-09-984-056-47	Sequence 47, Appl	473	3	75.0	19	10	US-09-864-761-42912	Sequence 42912, A
401	3	75.0	9	10	US-09-984-057-47	Sequence 47, Appl	474	3	75.0	19	10	US-09-864-761-45839	Sequence 45839, A
402	3	75.0	9	12	US-10-062-257-12	Sequence 12, Appl	475	3	75.0	19	10	US-09-766-412-49	Sequence 49, Appl
403	3	75.0	10	8	US-08-854-825-28	Sequence 28, Appl	476	3	75.0	19	10	US-09-766-412-50	Sequence 50, Appl
404	3	75.0	10	9	US-09-824-787B-95	Sequence 95, Appl	477	3	75.0	19	12	US-10-071-751-87	Sequence 87, Appl
405	3	75.0	10	9	US-10-121-415-1	Sequence 1, Appl	478	3	75.0	20	8	US-08-424-550B-280	Sequence 280, App
406	3	75.0	10	9	US-09-924-400-312	Sequence 312, App	479	3	75.0	20	9	US-10-029-009-12	Sequence 12, Appl
407	3	75.0	10	10	US-09-729-835-73	Sequence 73, Appl	480	3	75.0	20	10	US-09-864-761-36958	Sequence 36958, A
408	3	75.0	10	10	US-09-870-162A-41	Sequence 41, Appl	481	3	75.0	20	10	US-09-864-761-44324	Sequence 44324, A
409	3	75.0	10	10	US-09-870-162A-42	Sequence 42, Appl	482	3	75.0	20	10	US-09-841-132-245	Sequence 245, App
410	3	75.0	10	10	US-09-810-936-312	Sequence 312, App	483	3	75.0	20	10	US-09-841-132-246	Sequence 246, App
411	3	75.0	10	10	US-09-780-053-181	Sequence 181, App	484	3	75.0	20	10	US-09-841-132-247	Sequence 247, App
412	3	75.0	10	10	US-09-780-053-305	Sequence 305, App	485	3	75.0	20	10	US-09-772-719-52	Sequence 52, Appl
413	3	75.0	10	10	US-09-780-053-705	Sequence 705, App	486	3	75.0	21	9	US-10-029-009-24	Sequence 24, Appl
414	3	75.0	10	10	US-09-429-755-312	Sequence 312, App	487	3	75.0	21	9	US-09-909-460-15	Sequence 15, Appl
415	3	75.0	10	10	US-09-894-018-324	Sequence 324, App	488	3	75.0	21	10	US-09-864-761-42534	Sequence 42534, A
416	3	75.0	11	12	US-10-007-761-5	Sequence 5, Appl	489	3	75.0	21	10	US-09-864-761-46599	Sequence 46599, A
417	3	75.0	11	10	US-09-734-520-63	Sequence 63, Appl	490	3	75.0	21	10	US-09-766-378A-36	Sequence 36, Appl
418	3	75.0	11	10	US-09-734-520-64	Sequence 64, Appl	491	3	75.0	21	10	US-09-853-830-30	Sequence 30, Appl
419	3	75.0	11	10	US-09-734-520-65	Sequence 65, Appl	492	3	75.0	21	12	US-10-001-879-152	Sequence 152, App
420	3	75.0	11	10	US-09-734-520-66	Sequence 66, Appl	493	3	75.0	22	9	US-09-310-113-7	Sequence 7, Appl
421	3	75.0	11	10	US-09-734-520-67	Sequence 67, Appl	494	3	75.0	22	10	US-09-815-136-11	Sequence 11, Appl
422	3	75.0	11	10	US-09-734-520-68	Sequence 68, Appl	495	3	75.0	22	10	US-09-847-185-6	Sequence 6, Appl
423	3	75.0	11	12	US-09-734-520-121	Sequence 121, App	496	3	75.0	23	9	US-09-975-143-31	Sequence 31, Appl
424	3	75.0	11	12	US-10-012-034A-63	Sequence 63, Appl	497	3	75.0	23	9	US-09-766-889A-12	Sequence 12, Appl
425	3	75.0	11	12	US-10-012-034A-64	Sequence 64, Appl	498	3	75.0	23	10	US-09-864-675-16	Sequence 16, Appl
426	3	75.0	11	12	US-10-012-034A-65	Sequence 65, Appl	499	3	75.0	24	10	US-09-864-761-37327	Sequence 37327, A
427	3	75.0	11	12	US-10-012-034A-66	Sequence 66, Appl	500	3	75.0	24	10	US-09-864-761-46629	Sequence 46629, A
428	3	75.0	11	12	US-10-012-034A-67	Sequence 67, Appl	501	3	75.0	24	10	US-09-883-727A-118	Sequence 118, App
429	3	75.0	11	12	US-10-012-034A-68	Sequence 68, Appl	502	3	75.0	24	10	US-09-764-847-623	Sequence 623, App
430	3	75.0	11	12	US-10-012-034A-121	Sequence 121, App	503	3	75.0	24	10	US-09-925-300-1837	Sequence 1837, App
431	3	75.0	11	12	US-10-010-310-1	Sequence 1, Appl	504	3	75.0	25	10	US-09-821-984-18	Sequence 18, Appl
432	3	75.0	12	9	US-10-050-189A-13	Sequence 13, Appl	505	3	75.0	25	10	US-09-215-077A-1	Sequence 1, Appl
433	3	75.0	12	10	US-09-888-721-17	Sequence 17, Appl	506	3	75.0	25	10	US-09-864-761-42413	Sequence 42413, A
434	3	75.0	12	10	US-09-071-838-8	Sequence 8, Appl	507	3	75.0	25	10	US-09-864-761-43058	Sequence 43058, A
435	3	75.0	13	10	US-09-888-721-16	Sequence 16, Appl	508	3	75.0	25	10	US-09-864-761-48412	Sequence 48412, A
436	3	75.0	13	12	US-10-001-843-187	Sequence 187, App	509	3	75.0	25	10	US-09-262-213A-1	Sequence 1, Appl
437	3	75.0	14	9	US-09-826-290-193	Sequence 193, App	510	3	75.0	26	10	US-09-864-761-35433	Sequence 35433, A
438	3	75.0	14	9	US-09-953-031A-2	Sequence 2, Appl	511	3	75.0	26	10	US-09-864-761-45015	Sequence 45015, A
439	3	75.0	14	9	US-09-953-031A-15	Sequence 15, Appl	512	3	75.0	26	10	US-09-864-761-47415	Sequence 47415, A
440	3	75.0	14	12	US-09-741-171-5	Sequence 5, Appl	513	3	75.0	26	10	US-09-864-761-47492	Sequence 47492, A
441	3	75.0	14	12	US-10-010-310-4	Sequence 4, Appl	514	3	75.0	26	10	US-09-847-185-5	Sequence 5, Appl
442	3	75.0	15	9	US-10-029-009-14	Sequence 14, Appl	515	3	75.0	26	10	US-09-985-157-3	Sequence 3, Appl
443	3	75.0	15	10	US-09-214-371-8	Sequence 8, Appl	516	3	75.0	27	10	US-09-864-761-34733	Sequence 34733, A
444	3	75.0	15	10	US-09-214-371-29	Sequence 29, Appl	517	3	75.0	27	10	US-09-864-761-38495	Sequence 38495, A
445	3	75.0	15	10	US-09-820-893-118	Sequence 118, App	518	3	75.0	27	10	US-09-864-761-41984	Sequence 41984, A
446	3	75.0	15	10	US-09-953-510-75	Sequence 75, App	519	3	75.0	27	10	US-09-985-157-2	Sequence 2, Appl
447	3	75.0	15	1	US-09-953-510-76	Sequence 76, Appl	520	3	75.0	28	9	US-09-908-153B-49	Sequence 49, Appl
448	3	75.0	16	1	US-08-918-189-2	Sequence 2, Appl	521	3	75.0	28	10	US-09-864-761-35924	Sequence 35924, A
449	3	75.0	16	9	US-10-029-009-26	Sequence 26, App	522	3	75.0	28	10	US-09-864-761-39762	Sequence 39762, A
450	3	75.0	16	10	US-10-016-634A-129	Sequence 129, App	523	3	75.0	28	10	US-09-864-761-41850	Sequence 41850, A
451	3	75.0	16	10	US-09-729-873-2	Sequence 2, Appl	524	3	75.0	28	10	US-09-864-761-44241	Sequence 44241, A
452	3	75.0	16	10	US-09-822-682-6	Sequence 6, Appl	525	3	75.0	28	10	US-09-864-761-45199	Sequence 45199, A
453	3	75.0	16	10	US-09-071-838-291	Sequence 291, App	526	3	75.0	28	10	US-09-864-761-46244	Sequence 46244, A
454	3	75.0	17	10	US-09-821-984-1	Sequence 1, Appl	527	3	75.0	28	10	US-09-827-998-12	Sequence 12, Appl
455	3	75.0	17	10	US-09-864-761-45910	Sequence 45910, A	528	3	75.0	28	10	US-09-922-261-271	Sequence 271, App
456	3	75.0	18	9	US-09-982-445-9	Sequence 9, Appl	529	3	75.0	28	10	US-09-071-838-97	Sequence 97, Appl
457	3	75.0	18	10	US-09-864-761-41659	Sequence 41659, A	530	3	75.0	29	10	US-09-818-878-54	Sequence 54, Appl

531	3	75.0	29	10	US-09-211-755B-54	Sequence 54, Appl	604	3	75.0	37	10	US-09-864-761-39452	Sequence 39452, A
532	3	75.0	29	10	US-09-782-980-158	Sequence 158, App	605	3	75.0	37	10	US-09-864-761-44363	Sequence 44363, A
533	3	75.0	29	10	US-09-764-877-1395	Sequence 1395, Ap	606	3	75.0	37	10	US-09-864-761-46802	Sequence 46802, A
534	3	75.0	29	10	US-09-867-852-17	Sequence 17, Appl	607	3	75.0	37	10	US-09-864-761-47199	Sequence 47199, A
535	3	75.0	30	10	US-09-864-761-35544	Sequence 35544, A	608	3	75.0	37	10	US-09-864-761-48352	Sequence 48352, A
536	3	75.0	30	10	US-09-864-761-35595	Sequence 35595, A	609	3	75.0	37	10	US-09-071-839-118	Sequence 118, App
537	3	75.0	30	10	US-09-864-761-35755	Sequence 35755, A	610	3	75.0	38	9	US-10-001-876-207	Sequence 207, App
538	3	75.0	30	10	US-09-864-761-43714	Sequence 43714, A	611	3	75.0	38	10	US-09-798-029-22	Sequence 22, Appl
539	3	75.0	30	10	US-09-925-297-541	Sequence 541, App	612	3	75.0	38	10	US-09-864-761-33530	Sequence 33530, A
540	3	75.0	30	10	US-09-917-340-23	Sequence 23, Appl	613	3	75.0	38	10	US-09-864-761-42714	Sequence 42714, A
541	3	75.0	30	10	US-09-732-091-16	Sequence 16, Appl	614	3	75.0	38	10	US-09-864-761-43643	Sequence 43643, A
542	3	75.0	30	10	US-09-935-494-70	Sequence 9, Appl	615	3	75.0	38	10	US-09-764-866-417	Sequence 117, Ap
543	3	75.0	30	12	US-10-038-045-9	Sequence 3, Appl	616	3	75.0	38	10	US-09-764-866-1113	Sequence 113, App
544	3	75.0	31	9	US-10-067-761-31	Sequence 3617, A	617	3	75.0	39	9	US-09-843-676-23	Sequence 1308, Ap
545	3	75.0	31	10	US-09-864-761-36617	Sequence 36617, A	618	3	75.0	39	9	US-09-843-676-23	Sequence 23, Appl
546	3	75.0	31	10	US-09-864-761-49080	Sequence 49080, A	619	3	75.0	39	9	US-10-050-1894-11	Sequence 11, Appl
547	3	75.0	31	10	US-09-804-156-31	Sequence 31, Appl	620	3	75.0	39	9	US-09-766-253-23	Sequence 23, Appl
548	3	75.0	31	10	US-09-782-980-140	Sequence 140, App	621	3	75.0	39	10	US-09-764-887-263	Sequence 263, App
549	3	75.0	32	9	US-09-989-919-80	Sequence 80, Appl	622	3	75.0	39	10	US-09-864-761-33428	Sequence 33428, A
550	3	75.0	32	10	US-09-864-761-34495	Sequence 34495, A	623	3	75.0	39	10	US-09-864-761-35025	Sequence 35025, A
551	3	75.0	32	10	US-09-864-761-37076	Sequence 37076, A	624	3	75.0	39	10	US-09-864-761-35446	Sequence 35446, A
552	3	75.0	32	10	US-09-864-761-39768	Sequence 39768, A	625	3	75.0	39	10	US-09-864-761-35659	Sequence 35659, A
553	3	75.0	32	10	US-09-864-761-46956	Sequence 46956, A	626	3	75.0	39	10	US-09-864-761-41697	Sequence 41697, A
554	3	75.0	32	10	US-09-864-761-48632	Sequence 48632, A	627	3	75.0	39	10	US-09-864-761-43205	Sequence 43205, A
555	3	75.0	32	10	US-09-281-717-23	Sequence 23, Appl	628	3	75.0	39	10	US-09-864-761-44556	Sequence 44556, A
556	3	75.0	32	10	US-09-922-261-157	Sequence 157, App	629	3	75.0	39	10	US-09-864-761-45103	Sequence 45103, A
557	3	75.0	32	10	US-09-922-261-281	Sequence 281, App	630	3	75.0	39	10	US-09-864-761-48402	Sequence 48402, A
558	3	75.0	32	10	US-09-764-847-650	Sequence 650, App	631	3	75.0	39	10	US-09-764-866-756	Sequence 756, App
559	3	75.0	32	10	US-09-982-172-230	Sequence 230, App	632	3	75.0	39	10	US-09-764-866-1050	Sequence 1050, Ap
560	3	75.0	33	9	US-09-984-245-92	Sequence 292, App	633	3	75.0	40	10	US-09-741-171-3	Sequence 3, Appl
561	3	75.0	33	10	US-09-767-395-27	Sequence 27, Appl	634	3	75.0	40	10	US-09-864-761-33670	Sequence 33670, A
562	3	75.0	33	10	US-09-864-761-44892	Sequence 44892, A	635	3	75.0	40	10	US-09-864-761-45072	Sequence 45072, A
563	3	75.0	33	10	US-09-864-761-45229	Sequence 45229, A	636	3	75.0	40	10	US-09-864-761-45670	Sequence 1127, Ap
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566	3	75.0	33	10	US-09-864-761-49019	Sequence 49019, A	639	3	75.0	41	10	US-09-726-643-92	Sequence 92, Appl
567	3	75.0	33	10	US-09-796-202-6	Sequence 6, Appl	640	3	75.0	41	10	US-09-864-761-34536	Sequence 34536, A
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576	3	75.0	34	10	US-09-864-761-38139	Sequence 38139, A	649	3	75.0	42	9	US-10-001-876-192	Sequence 192, App
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697	3	75.0	45	10	US-09-925-299-1399	Sequence 1399, Ap	770	3	75.0	52	10	US-09-764-847-616	Sequence 616, App
698	3	75.0	45	10	US-09-789-561-114	Sequence 114, App	771	3	75.0	52	12	US-10-040-916-39	Sequence 39, Appl
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705	3	75.0	46	10	US-09-864-761-40960	Sequence 40960, A	778	3	75.0	53	10	US-09-764-869-910	Sequence 910, App
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707	3	75.0	46	10	US-09-764-860-375	Sequence 375, App	780	3	75.0	53	10	US-09-925-300-1523	Sequence 1523, Ap
708	3	75.0	46	10	US-09-508-322-52	Sequence 52, Appl	781	3	75.0	54	9	US-10-001-876-173	Sequence 173, App
709	3	75.0	46	10	US-09-764-877-1297	Sequence 1297, Ap	782	3	75.0	54	10	US-09-864-761-46979	Sequence 46979, A
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712	3	75.0	47	10	US-09-224-683-64	Sequence 64, Appl	785	3	75.0	54	10	US-09-764-877-1324	Sequence 1324, Ap
713	3	75.0	47	10	US-09-925-302-510	Sequence 510, App	786	3	75.0	55	9	US-10-012-896-566	Sequence 566, App
714	3	75.0	47	10	US-09-925-302-740	Sequence 740, App	787	3	75.0	55	9	US-09-895-793-566	Sequence 566, App
715	3	75.0	47	10	US-09-864-761-35916	Sequence 35916, A	788	3	75.0	55	9	US-09-895-814-566	Sequence 566, App
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722	3	75.0	47	10	US-09-982-172-14	Sequence 14, Appl	795	3	75.0	55	10	US-09-822-827-566	Sequence 566, App
723	3	75.0	47	10	US-09-982-172-213	Sequence 213, App	796	3	75.0	55	10	US-09-867-550-770	Sequence 770, App
724	3	75.0	48	10	US-09-739-907-72	Sequence 72, Appl	797	3	75.0	56	9	US-09-764-877-1761	Sequence 1761, Ap
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730	3	75.0	48	10	US-10-001-870-122	Sequence 122, App	803	3	75.0	56	10	US-09-867-550-208	Sequence 208, App
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732	3	75.0	49	9	US-09-764-868-1212	Sequence 1212, Ap	805	3	75.0	56	10	US-09-764-877-1310	Sequence 1310, Ap
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736	3	75.0	49	10	US-09-864-761-39876	Sequence 39876, A	809	3	75.0	57	10	US-09-764-887-246	Sequence 246, App
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740	3	75.0	49	10	US-09-764-855-143	Sequence 143, App	813	3	75.0	57	10	US-09-864-761-43407	Sequence 43407, A
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746	3	75.0	50	10	US-09-864-761-42504	Sequence 42504, A	819	3	75.0	57	10	US-09-867-550-148	Sequence 148, App
747	3	75.0	50	10	US-09-925-301-1565	Sequence 1565, Ap	820	3	75.0	58	9	US-10-029-191-7	Sequence 7, Appl
748	3	75.0	50	10	US-09-867-550-1486	Sequence 1486, Ap	821	3	75.0	58	9	US-09-981-876-190	Sequence 190, App
749	3	75.0	50	10	US-09-911-826A-15	Sequence 15, Appl	822	3	75.0	58	9	US-09-989-919-114	Sequence 114, App



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832	3	75.0	58	10	US-09-867-550-254	Sequence 254, App	905	3	75.0	62	10	US-09-805-204-13	Sequence 13, App1
833	3	75.0	58	10	US-09-764-878-191	Sequence 191, App	906	3	75.0	63	9	US-09-764-877-699	Sequence 699, App
834	3	75.0	58	10	US-09-970-108-2	Sequence 2, App1	907	3	75.0	63	9	US-10-061-396-23	Sequence 23, App1
835	3	75.0	59	9	US-09-796-692-1302	Sequence 1302, App	908	3	75.0	63	10	US-09-843-885-29	Sequence 29, App1
836	3	75.0	59	9	US-09-796-692-2293	Sequence 2293, App	909	3	75.0	63	10	US-09-864-761-37449	Sequence 37449, App
837	3	75.0	59	10	US-09-864-761-34914	Sequence 34914, A	910	3	75.0	63	10	US-09-864-761-40865	Sequence 40865, A
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839	3	75.0	59	10	US-09-864-761-40052	Sequence 40052, A	912	3	75.0	63	10	US-09-925-299-1285	Sequence 1285, App
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842	3	75.0	59	10	US-09-925-299-1267	Sequence 1267, App	915	3	75.0	63	10	US-09-877-1437	Sequence 1437, App
843	3	75.0	59	10	US-09-867-550-460	Sequence 460, App	916	3	75.0	64	8	US-09-764-877-1583	Sequence 1583, App
844	3	75.0	59	10	US-09-935-428A-7	Sequence 7, App1	917	3	75.0	64	8	US-08-873-601-22	Sequence 22, App1
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## ALIGNMENTS

RESULT 1  
US-09-867-847-15  
; Sequence 15, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-15

Query Match 100.0%; Score 4; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
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Db 1 KLVF 4

RESULT 2  
US-09-867-847-23  
; Sequence 23, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
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; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
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; OTHER INFORMATION: or peptidomimetics  
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; LOCATION: (4)  
; OTHER INFORMATION: AMIDATION  
US-09-867-847-23

Query Match 100.0%; Score 4; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
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Db 1 KLVF 4

RESULT 3  
US-09-850-061A-25  
; Sequence 25, Application US/09850061A  
; Patent No. US20020094957A1  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: THYBERG, Johan  
; APPLICANT: TJERNBERG, Lars O.  
; APPLICANT: TERENIUS, Lars  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 03315-002  
; CURRENT APPLICATION NUMBER: US/09/850,061A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 09/095,106  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
; PRIOR FILING DATE: 1996-12-09  
; PRIOR APPLICATION NUMBER: SE 9504467-3  
; PRIOR FILING DATE: 1995-12-12  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Amyloidosis  
US-09-850-061A-25

Query Match 100.0%; Score 4; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 1 KLVF 4

RESULT 4  
US-09-867-847-17  
; Sequence 17, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiang  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 1445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-17

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Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 1 KLVF 4

RESULT 5  
US-09-867-847-25  
; Sequence 25, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiang  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 1445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides

; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD RES  
; LOCATION: (5)  
; OTHER INFORMATION: AMIDATION  
US-09-867-847-25

Query Match 100.0%; Score 4; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
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Db 1 KLVF 4

RESULT 6  
US-09-850-061A-1  
; Sequence 1, Application US/09850061A  
; Patent No. US20020094957A1  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: TYRBERG, Johan  
; APPLICANT: TERNERUS, Lars O.  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 03315-002  
; CURRENT APPLICATION NUMBER: US/09/850,061A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 09/095,106  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
; PRIOR FILING DATE: 1996-12-09  
; PRIOR APPLICATION NUMBER: SE 9504467-3  
; PRIOR FILING DATE: 1995-12-12  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Amyloidosis  
US-09-850-061A-1

Query Match 100.0%; Score 4; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 1 KLVF 4

RESULT 7  
US-09-850-061A-19  
; Sequence 19, Application US/09850061A  
; Patent No. US20020094957A1  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: TYRBERG, Johan  
; APPLICANT: TERNERUS, Lars O.  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 03315-002  
; CURRENT APPLICATION NUMBER: US/09/850,061A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 09/095,106  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
; PRIOR FILING DATE: 1996-12-09  
; PRIOR APPLICATION NUMBER: SE 9504467-3

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; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-19

Query Match      100.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 2 KLVF 5

RESULT 8
US-09-850-061A-43
; Sequence 43, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERNETUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850.061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-43

Query Match      100.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 1 KLVF 4

RESULT 9
US-09-972-475-10
; Sequence 10, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

Qy 1 KLVF 4
Db 1 KLVF 4

RESULT 9
US-09-972-475-10
; Sequence 10, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PFI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-972-475-10

Query Match      100.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 1 KLVF 4

RESULT 10
US-09-972-475-37
; Sequence 37, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
```

```

?      REGISTRATION NUMBER: 31,503
?      REFERENCE/DOCKET NUMBER: PPI-002C22
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (617)227-7400
?      TELEFAX: (617)227-5941
?      INFORMATION FOR SEQ ID NO: 37:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 5 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: peptide
?      FRAGMENT TYPE: internal
?      SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-972-475-37

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Query Match      100.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	KLVF	4
Db	2	KLVF	5

RESULT 11  
US-09-867-847-7  
; Sequence 7, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION.

```

? APPLICANT: Gervais, Francine
? TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
? TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
? FILE REFERENCE: 14445-501 CIP
? CURRENT APPLICATION NUMBER: US/09/867,847
? PRIORITY FILING DATE: 2001-09-20
? PRIOR APPLICATION NUMBER: 60/168,594
? PRIORITY FILING DATE: 1999-11-29
? PRIOR APPLICATION NUMBER: 09/724,842
? PRIORITY FILING DATE: 2000-11-28
? NUMBER OF SEQ ID NOS: 65
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO: 7
? LENGTH: 6
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: All D peptides
? IS-09-867-847-7

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Query Match	100.0%	Score 4	DB 10	Length 6
Best Local Similarity	100.0%	Pred. No.	9.8e+04	
Matches	4	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	1	KLVF	4	
db	1	KLVF	4	

RESULT 12  
US-09-867-847-20  
; Sequence 20, Application US/09867847  
; Patent No. US20020094335A1  
GENERAL INFORMATION

; APPLICANT: Hebert, lise  
 ; APPLICANT: Kong, Xiangl  
 ; APPLICANT: Gervais, Francine  
 ; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
 ; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES

```

1 FILE REFERENCE: 14445-501 CIP
2 CURRENT APPLICATION NUMBER: US/09/867, 847
3 CURRENT FILING DATE: 2001-09-20
4 PRIOR APPLICATION NUMBER: 60/168, 594
5 PRIOR FILING DATE: 1999-11-29
6 PRIOR APPLICATION NUMBER: 09/724, 842
7 PRIOR FILING DATE: 2000-11-28
8 NUMBER OF SEQ ID NOS: 65
9 SOFTWARE: PatentIn Ver. 2.1
10 SEQ ID NO 20
11
12 LENGTH: 6
13
14 TYPE: PRT
15
16 ORGANISM: Artificial Sequence
17
18 FEATURE:
19
20 OTHER INFORMATION: Description of Artificial Sequence: All D peptides
21
22 OTHER INFORMATION: or Peptidomimetics
23
24 NAME/KEY: MOD_RES
25
26 LOCATION: (6)-
27
28 OTHER INFORMATION: AMIDATION
29
30 US-09-867-847-20

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Query Match	100.0%;	Score 4;	DB 10;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 9.8e+04;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	KLVF	4
Db	1	KLVF	4

RESULT 13  
US-09-867-847-52  
; Sequence 52, Application US/09867847  
; Patent No. US2002009435A1  
GENERAL INFORMATION

```

? APPLICANT: Gervais, Francine
? TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
? TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
? FILE REFERENCE: 14445-501 CIP
? CURRENT APPLICATION NUMBER: US/09/867,847
? CURRENT FILING DATE: 2001-09-20
? PRIOR APPLICATION NUMBER: 60/168,594
? PRIOR FILING DATE: 1999-11-29
? PRIOR APPLICATION NUMBER: 09/724,842
? PRIOR FILING DATE: 2000-11-28
? NUMBER OF SEQ ID NOS: 65
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 52
? LENGTH: 6
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: All D peptides
? OTHER INFORMATION: or peptidomimetics
? US-09-867-847-52

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Query Match	100.0%;	Score 4;	DB 10;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 9.8e+04;		
Matches	4;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	.1	KLVF	4
Db	1	KLVF	4

RESULT 14  
US-09-867-847-55  
; Sequence 55, Application US/09867847  
; Patent No. US20080094335A1  
; GENERAL INFORMATION:

; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
US-09-867-847-55

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 15  
US-09-867-847-58  
; Sequence 58, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 58  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)..(5)  
; OTHER INFORMATION: Xaa is thienylalanine  
US-09-867-847-58

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 16  
US-09-867-847-61  
; Sequence 61, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Xaa is cyclohexylalanine  
US-09-867-847-61

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 1 KLVF 4

RESULT 17  
US-09-867-847-64  
; Sequence 64, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalifour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 64  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)  
; OTHER INFORMATION: Xaa is phenylglycine  
US-09-867-847-64

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 1 KLVF 4

RESULT 18  
US-09-850-061A-5  
; Sequence 5, Application US/09850061A  
; Patent No. US20020094957A1  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: TYRBERG, Johan  
; APPLICANT: TYRBERG, Lars O.  
; APPLICANT: TYRBERG, Lars O.  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 033315-002  
; CURRENT APPLICATION NUMBER: US/09/850,061A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 09/095,106  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
; PRIOR FILING DATE: 1996-12-09  
; PRIOR APPLICATION NUMBER: SE 9504467-3  
; PRIOR FILING DATE: 1995-12-12  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Amyloidosis  
US-09-850-061A-5

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 2 KLVF 5

RESULT 19  
US-09-850-061A-15  
; Sequence 15, Application US/09850061A  
; Patent No. US20020094957A1  
; GENERAL INFORMATION:  
; APPLICANT: NORDSTEDT, Christer  
; APPLICANT: NASLUND, Jan  
; APPLICANT: TYRBERG, Johan  
; APPLICANT: TYRBERG, Lars O.  
; APPLICANT: TYRBERG, Lars O.  
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
; FILE REFERENCE: 033315-002  
; CURRENT APPLICATION NUMBER: US/09/850,061A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 09/095,106  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
; PRIOR FILING DATE: 1996-12-09  
; PRIOR APPLICATION NUMBER: SE 9504467-3  
; PRIOR FILING DATE: 1995-12-12  
; PRIOR APPLICATION NUMBER: US 60/009,386  
; PRIOR FILING DATE: 1995-12-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Amyloidosis  
US-09-850-061A-15

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 3 KLVF 6

RESULT 20  
US-09-972-475-8  
; Sequence 8, Application US/09972475  
; Patent No. US20020098173A1  
; GENERAL INFORMATION:  
; APPLICANT: Findels, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/972,475  
; FILING DATE: 04-Oct-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,267  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: USN 08/475,579  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-972-475-8

Query Match 100.0%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
Db 2 KLVF 5

RESULT 21  
US-09-972-475-9  
; Sequence 9, Application US/09972475

```
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-7400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9
Query Match 100.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVF 4
Db 1 KLVF 4
RESULT 22
US-09-972-475-31
; Sequence 31, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-7400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9
Query Match 100.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVF 4
Db 1 KLVF 4
RESULT 22
US-09-972-475-31
; Sequence 31, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-7400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-31
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; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-972-475-31
Query Match 100.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVF 4
Db 1 KLVF 4
RESULT 23
US-09-972-475-43
; Sequence 43, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 6
; OTHER INFORMATION: /note= Xaa is beta-alanyl
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-972-475-31
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; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 43:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 6 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
;   SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-972-475-43

Query Match          100.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 2 KLVF 5

RESULT 24
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match          100.0%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 1 KLVF 4

RESULT 25
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-12

Query Match          100.0%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 2 KLVF 5

RESULT 26
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-27

Query Match          100.0%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 1 KLVF 4

RESULT 27
US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
```

```
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match          100.0%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 1 KLVF 4

RESULT 28
US-09-850-061A-11
; Sequence 11, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: THYBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850,061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-11

Query Match          100.0%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 3 KLVF 6

RESULT 29
US-09-850-061A-12
; Sequence 12, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: THYBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850,061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-11

Query Match          100.0%; Score 4; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 3 KLVF 6

RESULT 30
US-09-972-475-6
; Sequence 6, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PP1-002CF2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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US-09-972-475-6

Query Match 100.0%; Score 4; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 3 KLVF 6

RESULT 31

US-09-972-475-7  
 ; Sequence 7, Application US/09972475  
 ; Patent No. US20020098173A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Findeis, Mark A. et al.  
 ; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
 ; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/972,475  
 ; FILING DATE: 04-Oct-2001  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/617,267  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: US98 08/475,579  
 ; FILING DATE: 07-JUN-1995  
 ; APPLICATION NUMBER: US98 08/548,998  
 ; FILING DATE: 27-OCT-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeConti, Giulio A.  
 ; REGISTRATION NUMBER: 31,503  
 ; REFERENCE/DOCKET NUMBER: PPI-002CP2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)227-5941  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 ; US-09-972-475-7

Query Match 100.0%; Score 4; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 2 KLVF 5

RESULT 32

US-09-850-061A-8  
 ; Sequence 8, Application US/09850061A  
 ; Patent No. US20020094957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NORDSTEDT, Christer  
 ; APPLICANT: NASLUND, Jan

; APPLICANT: THYBERG, Johan  
 ; APPLICANT: TURNBERG, Lars O.

; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
 ; FILE REFERENCE: 03315-002  
 ; CURRENT APPLICATION NUMBER: US/09/850,061A  
 ; CURRENT FILING DATE: 2001-05-08  
 ; PRIOR APPLICATION NUMBER: US 09/095,106  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
 ; PRIOR FILING DATE: 1996-12-09  
 ; PRIOR APPLICATION NUMBER: SE 9504467-3  
 ; PRIOR FILING DATE: 1995-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/009,386  
 ; PRIOR FILING DATE: 1995-12-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 8  
 ; TYPE: PPT  
 ; ORGANISM: Amyloidosis  
 ; US-09-850-061A-8

Query Match 100.0%; Score 4; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 4 KLVF 7

RESULT 33

US-09-850-061A-9  
 ; Sequence 9, Application US/09850061A  
 ; Patent No. US20020094957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NORDSTEDT, Christer  
 ; APPLICANT: NASLUND, Jan  
 ; APPLICANT: THYBERG, Johan  
 ; APPLICANT: TURNBERG, Lars O.  
 ; APPLICANT: TURNERUS, Lars  
 ; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA  
 ; FILE REFERENCE: 03315-002  
 ; CURRENT APPLICATION NUMBER: US/09/850,061A  
 ; CURRENT FILING DATE: 2001-05-08  
 ; PRIOR APPLICATION NUMBER: US 09/095,106  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: PCT/SE96/01621  
 ; PRIOR FILING DATE: 1996-12-09  
 ; PRIOR APPLICATION NUMBER: SE 9504467-3  
 ; PRIOR FILING DATE: 1995-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/009,386  
 ; PRIOR FILING DATE: 1995-12-29  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 8  
 ; TYPE: PPT  
 ; ORGANISM: Amyloidosis  
 ; US-09-850-061A-9

Query Match 100.0%; Score 4; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 5 KLVF 8

RESULT 34

US-09-850-061A-44

```
; Sequence 44, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TURNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850.061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-44

Query Match      100.0%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVF 4
      ||||
Db      1 KLVF 4

RESULT 35
US-09-972-475-5
; Sequence 5, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
```

```
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-972-475-5

Query Match      100.0%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVF 4
      ||||
Db      3 KLVF 6

RESULT 36
US-09-899-815-2
; Sequence 2, Application US/09899815
; Patent No. US20020162129A1
; GENERAL INFORMATION:
; APPLICANT: LANNFELT, Lars
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: LANNFELT-1A
; CURRENT APPLICATION NUMBER: US/09/899,815
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,098
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: EP 00202387.7
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (16-24 of SEQ ID NO:1)
US-09-899-815-2

Query Match      100.0%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KLVF 4
      ||||
Db      1 KLVF 4

RESULT 37
US-09-867-847-9
; Sequence 9, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
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```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-9
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```
Query Match          100.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 KLVF 4
        ||||
Db       4 KLVF 7
```

```
RESULT 38
US-09-850-061A-6
; Sequence 6, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TERNBERG, Lars O.
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850,061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-6
```

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Query Match          100.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 KLVF 4
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Db       5 KLVF 8
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RESULT 39
US-09-850-061A-7
; Sequence 7, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TERNBERG, Lars O.
; APPLICANT: TERNBERG, Lars O.
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850,061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
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; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-850-061A-7
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Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       6 KLVF 9
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US-09-867-847-29
; Sequence 29, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangq
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-29
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Query Match          100.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 KLVF 4
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Db       4 KLVF 7
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Search completed: January 3, 2003, 08:00:24  
Job time : 12 secs



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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:48:11 ; Search time 15 Seconds  
(without alignments)  
25.636 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 4

Sequence: 1 KLVF 4

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	4	100.0	29	C47719	T-cell receptor al
4	4	100.0	30	E31461	T-cell receptor de
5	4	100.0	31	F31461	T-cell receptor de
6	4	100.0	32	D32502	T-cell receptor de
7	4	100.0	32	A32502	T-cell receptor de
8	4	100.0	32	D31461	T-cell receptor de
9	4	100.0	33	B32540	T-cell receptor de
10	4	100.0	33	E32502	T-cell receptor de
11	4	100.0	33	F31461	T-cell receptor de
12	4	100.0	33	A31461	T-cell receptor de
13	4	100.0	33	B31461	T-cell receptor de
14	4	100.0	33	S23094	beta-amyloid prote
15	4	100.0	34	I32502	T-cell receptor de
16	4	100.0	34	C31461	T-cell receptor de
17	4	100.0	34	H31461	T-cell receptor de
18	4	100.0	36	H32502	T-cell receptor de
19	4	100.0	36	A32540	T-cell receptor de
20	4	100.0	36	C32502	T-cell receptor de
21	4	100.0	42	PN0512	beta-amyloid prote
22	4	100.0	47	PC4133	hypothetical 47 pr
23	4	100.0	53	PS0009	glycylcinn Alab1b pr
24	4	100.0	57	B60045	Alzheimer's diseas
25	4	100.0	57	F60045	Alzheimer's diseas
26	4	100.0	57	G60045	Alzheimer's diseas
27	4	100.0	57	D60045	Alzheimer's diseas
28	4	100.0	57	A60045	Alzheimer's diseas
29	4	100.0	57	B60045	Alzheimer's diseas

30	4	100.0	57	2	D97742	hypothetical prote
31	4	100.0	67	2	B97758	hypothetical prote
32	4	100.0	69	2	B33979	peptidyl-dipectida
33	4	100.0	69	2	T46201	protein translocat
34	4	100.0	71	2	AB2884	hypothetical prote
35	4	100.0	72	2	S28793	major merozoite su
36	4	100.0	73	2	A38883	rab protein Rab6 -
37	4	100.0	75	2	S35774	T-cell receptor al
38	4	100.0	78	2	B84305	hypothetical prote
39	4	100.0	79	2	C97829	hypothetical prote
40	4	100.0	81	2	H71614	protein translocat
41	4	100.0	82	2	PQ0438	Alzheimer's diseas
42	4	100.0	83	2	AD2896	hypothetical prote
43	4	100.0	84	2	AC3376	hypothetical prote
44	4	100.0	86	1	PC4322	ribosomal protein
45	4	100.0	86	2	B44530	T-cell receptor al
46	4	100.0	90	2	H84410	hypothetical prote
47	4	100.0	90	2	D82760	hypothetical prote
48	4	100.0	91	2	B64413	hypothetical prote
49	4	100.0	91	2	H97796	RP534 protein homo
50	4	100.0	94	2	S61934	signal peptidase 1
51	4	100.0	95	1	BORR3	prostatic steroid-
52	4	100.0	96	2	T25103	hypothetical prote
53	4	100.0	97	2	D64600	conserved hypothet
54	4	100.0	97	2	C71913	hypothetical prote
55	4	100.0	99	2	F95064	ribosomal protein
56	4	100.0	99	2	H97931	conserved hypothet
57	4	100.0	100	2	F81836	transcription regu
58	4	100.0	100	2	AF0773	hypothetical prote
59	4	100.0	101	2	A11753	Orf47 (bacterioph
60	4	100.0	105	2	S42812	hydroxymethylgluta
61	4	100.0	105	2	S17345	hydroxymethylgluta
62	4	100.0	106	2	S43069	hypothetical prote
63	4	100.0	107	2	F86869	hypothetical prote
64	4	100.0	109	1	MNTRB2	nonstructural prot
65	4	100.0	109	1	A44275	nonstructural prot
66	4	100.0	109	2	S58182	nonstructural prot
67	4	100.0	109	2	S58186	nonstructural prot
68	4	100.0	110	2	A24092	T-cell receptor al
69	4	100.0	110	2	A24444	hypothetical prote
70	4	100.0	110	2	A11856	hypothetical prote
71	4	100.0	112	2	S73078	hypothetical prote
72	4	100.0	112	2	T47326	hypothetical prote
73	4	100.0	113	4	I39320	T cell receptor al
74	4	100.0	116	2	F72419	hypothetical prote
75	4	100.0	116	2	E90716	hypothetical prote
76	4	100.0	116	2	T05517	absicisic acid-indu
77	4	100.0	117	2	H71431	hypothetical prote
78	4	100.0	117	2	T13210	minor capsid prote
79	4	100.0	119	2	AC0080	probable dihydron
80	4	100.0	120	2	AE0892	T-cell receptor de
81	4	100.0	120	2	C26945	insertion sequence
82	4	100.0	121	2	S23781	ribosomal protein
83	4	100.0	122	1	S58649	cadmium-binding pr
84	4	100.0	122	2	E84154	hypothetical prote
85	4	100.0	122	2	S73009	hypothetical prote
86	4	100.0	122	2	AG1887	hypothetical prote
87	4	100.0	123	1	H65093	probable dihydron
88	4	100.0	123	1	E91121	probable kinase [l
89	4	100.0	123	2	D85966	probable kinase Y9
90	4	100.0	123	2	PL0032	T-cell receptor de
91	4	100.0	124	2	A70873	T-cell receptor al
92	4	100.0	126	2	H69267	probable trxa prot
93	4	100.0	127	1	CCR2V	cytochrome-c oxida
94	4	100.0	128	2	G86629	cytochrome c2 prec
95	4	100.0	128	2	AC3428	hypothetical prote
96	4	100.0	129	2	S78103	transposase BME14
97	4	100.0	130	2	D23774	T-cell receptor de
98	4	100.0	131	2	E24092	T-cell receptor al
99	4	100.0	131	2	D24092	T-cell receptor al
100	4	100.0	133	2	S49487	long-chain-fatty-a
101	4	100.0	133	2	S57886	T cell receptor al
102	4	100.0	133	2	G45893	T-cell receptor al

103	4	100.0	134	2	S57890	T cell receptor Hw	176	4	100.0	190	2	A59418	kunitz type subtil
104	4	100.0	135	2	T13489	T-cell receptor al	177	4	100.0	190	2	E64775	probable lipoprote
105	4	100.0	136	2	C90254	hypothetical prote	178	4	100.0	190	2	G90692	glycoprotein/polys
106	4	100.0	137	2	S03477	T-cell receptor al	179	4	100.0	190	2	G85542	glycoprotein/polys
107	4	100.0	139	2	A70426	8-OKO-dGTPase doma	180	4	100.0	191	2	E64376	membrane protein h
108	4	100.0	140	2	B95049	hypothetical prote	181	4	100.0	191	2	E30754	hypothetical prote
109	4	100.0	141	2	H97919	(3R)-hydroxymyrist	182	4	100.0	191	2	D90798	probable tellurium
110	4	100.0	142	2	FL0045	T-cell receptor al	183	4	100.0	191	2	E85607	probable tellurium
111	4	100.0	143	2	D95237	phosphotyrosine pr	184	4	100.0	193	1	RDBPT4	dihydrofolate redu
112	4	100.0	142	2	E98101	conserved hypotet	185	4	100.0	193	2	T29706	GTP-binding protei
113	4	100.0	142	2	D75134	hypothetical prote	186	4	100.0	194	2	S21859	hypothetical prote
114	4	100.0	143	2	JI0082	T-cell receptor de	187	4	100.0	194	2	F64025	hypothetical prote
115	4	100.0	144	2	B30471	hypothetical prote	188	4	100.0	194	2	T50787	hypothetical prote
116	4	100.0	144	2	A86722	hypothetical prote	189	4	100.0	198	2	S39543	GTP-binding protei
117	4	100.0	144	2	AC2572	hypothetical prote	190	4	100.0	198	2	F95139	hemolysin A, proba
118	4	100.0	146	2	B64246	ribosomal protein	191	4	100.0	199	2	E69756	tellurium resistan
119	4	100.0	146	2	B97426	flagellar protein	192	4	100.0	199	2	PQ0542	polyprotein - suga
120	4	100.0	146	2	AH2258	hypothetical prote	193	4	100.0	199	2	H72242	flagellar L-ring p
121	4	100.0	147	2	S76050	hypothetical prote	194	4	100.0	199	2	T20927	hypothetical prote
122	4	100.0	152	2	T06645	hypothetical prote	195	4	100.0	201	2	S12789	GTP-binding protei
123	4	100.0	152	2	F86473	hypothetical prote	196	4	100.0	201	2	C97074	terE family protei
124	4	100.0	156	1	B64021	hypothetical prote	197	4	100.0	201	2	F69988	hypothetical prote
125	4	100.0	157	2	E97424	hypothetical 18.7K	198	4	100.0	202	2	S21346	probable pol polyp
126	4	100.0	157	2	AD2642	conserved hypotet	199	4	100.0	203	2	JO1091	trypsin inhibitor
127	4	100.0	158	2	E86191	hypothetical prote	200	4	100.0	203	2	T02868	probable GTP-bindi
128	4	100.0	159	2	AD1742	protein involved i	201	4	100.0	203	2	T24042	hypothetical prote
129	4	100.0	159	2	AF1372	proteins involved	202	4	100.0	204	2	JO1092	trypsin inhibitor
130	4	100.0	159	2	H71845	hypothetical prote	203	4	100.0	204	2	S70149	DNA-invertase - Xa
131	4	100.0	159	2	A64672	hypothetical prote	204	4	100.0	204	2	T45948	hypothetical prote
132	4	100.0	159	2	H83279	hypothetical prote	205	4	100.0	205	2	S31127	GTP-binding protei
133	4	100.0	160	2	H83673	PTS system, galact	206	4	100.0	205	2	T34375	hypothetical prote
134	4	100.0	160	2	AE1485	hypothetical prote	207	4	100.0	206	2	JC7311	20K protein - soyb
135	4	100.0	162	2	AB2644	flagellar protein	208	4	100.0	207	2	H84610	probable GTP-bindi
136	4	100.0	164	2	D71846	ribosomal protein	209	4	100.0	207	2	T50814	GTP-binding protei
137	4	100.0	164	2	H64669	ribosomal protein	210	4	100.0	207	2	S32180	DNA-invertase - Kl
138	4	100.0	165	2	D90600	thiol peroxidase [	211	4	100.0	207	2	T08520	DNA-invertase - En
139	4	100.0	165	2	H97142	hypothetical prote	212	4	100.0	208	2	AF3538	uracil phosphoribo
140	4	100.0	166	2	D87664	hypothetical prote	213	4	100.0	208	2	S49196	Kunitz trypsin inh
141	4	100.0	166	2	D37844	baIE 19.5K protein	214	4	100.0	208	2	T03627	GTP-binding protei
142	4	100.0	167	2	A32646	peroxisomal membra	215	4	100.0	208	2	G34323	GTP-binding protei
143	4	100.0	169	2	G72121	ct303 hypothetical	216	4	100.0	208	2	T01588	GTP-binding protei
144	4	100.0	169	2	E86502	Ct303 hypothetical	217	4	100.0	208	2	F64244	ATP synthase B cha
145	4	100.0	169	2	B64806	ybgA protein - Esc	218	4	100.0	208	2	D64380	conserved hypotet
146	4	100.0	169	2	D90720	hypothetical prote	219	4	100.0	208	2	D88961	protein F59A7.6 [l
147	4	100.0	169	2	B85571	hypothetical prote	220	4	100.0	209	2	C87530	uracil phosphoribo
148	4	100.0	169	2	FC4143	hypothetical 169 p	221	4	100.0	209	2	C97375	uracil phosphoribo
149	4	100.0	170	2	G81375	hypothetical prote	222	4	100.0	209	2	AI2592	uracil phosphoribo
150	4	100.0	170	2	E70219	hypothetical prote	223	4	100.0	209	2	E98053	hypothetical prote
151	4	100.0	171	2	FC2038	smooth muscle prot	224	4	100.0	209	2	D95186	conserved hypotet
152	4	100.0	171	2	B87628	conserved hypotet	225	4	100.0	210	2	E87640	conserved hypotet
153	4	100.0	171	2	F90266	hypothetical prote	226	4	100.0	210	2	A85018	probable copper-co
154	4	100.0	171	2	D81278	probable periplasm	227	4	100.0	214	2	T06095	GTP-binding protei
155	4	100.0	172	2	C81549	conserved hypotet	228	4	100.0	214	2	T47892	hypothetical prote
156	4	100.0	175	2	G96535	hypothetical prote	229	4	100.0	215	2	S74602	hypothetical prote
157	4	100.0	176	1	E44056	22K protein - feli	230	4	100.0	215	2	F72412	hypothetical prote
158	4	100.0	176	2	A99234	gndp-4-dehydroxam	231	4	100.0	216	2	JO9568	trypsin inhibitor
159	4	100.0	176	2	G90357	hypothetical prote	232	4	100.0	216	2	AF1513	probable transaldo
160	4	100.0	176	2	T22614	hypothetical prote	233	4	100.0	216	2	T50314	probable human pop
161	4	100.0	179	2	S64843	hypothetical prote	234	4	100.0	217	1	TISY	trypsin inhibitor
162	4	100.0	181	1	TISYC	trypsin inhibitor	235	4	100.0	217	1	S19190	trypsin inhibitor
163	4	100.0	181	1	TISYB	trypsin inhibitor	236	4	100.0	217	2	F97405	GTP-binding protei
164	4	100.0	181	2	T36787	probable NTP pyrop	237	4	100.0	217	2	AG2623	GTP-binding protei
165	4	100.0	182	2	E75597	probable lipopolys	238	4	100.0	219	2	A64043	uracil-DNA glycosy
166	4	100.0	182	2	T40976	hypothetical prote	239	4	100.0	220	1	A33872	miraculin precurs
167	4	100.0	183	2	JK0311	kunitz type subtil	240	4	100.0	220	2	H81048	biopolymer transpo
168	4	100.0	183	2	S76453	hypothetical prote	241	4	100.0	220	2	C87601	glutathione S-tran
169	4	100.0	186	2	T06911	H+-transporting tw	242	4	100.0	222	2	T26213	hypothetical prote
170	4	100.0	186	2	T50672	probable zinc fing	243	4	100.0	224	1	WMVZR1	26.3K late gene tr
171	4	100.0	187	2	F71063	hypothetical prote	244	4	100.0	224	2	F71934	molybdate ABC tran
172	4	100.0	189	2	G89468	protein F07G6.7 [i	245	4	100.0	224	2	B64579	molybdenum ABC tra
173	4	100.0	189	2	AE0560	conserved hypotet	246	4	100.0	224	2	G72163	A2L protein - vari
174	4	100.0	190	2	JK0310	kunitz type subtil	247	4	100.0	224	2	C36848	A2L protein - vari
175	4	100.0	190	2	A59416	kunitz type subtil	248	4	100.0	224	2	T28543	hypothetical prote



249	4	100.0	224	2	T21896	hypothetical prote	322	4	100.0	280	2	D64239	lic-1 operon prote
250	4	100.0	226	2	E64013	probable phosphos	323	4	100.0	280	2	D97174	enzyme of lile/PAB
251	4	100.0	227	2	A64924	uncharacterized me	324	4	100.0	280	2	H89800	hypothetical prote
252	4	100.0	228	2	T30706	probable transacti	325	4	100.0	281	2	A12704	conserved hypotet
253	4	100.0	229	2	C69806	hypothetical prote	326	4	100.0	280	2	B54498	major merzoiite su
254	4	100.0	230	2	E95192	phosphoglycerate m	327	4	100.0	281	2	T32765	hypothetical prote
255	4	100.0	230	2	B98059	phosphoglycerate m	328	4	100.0	282	2	AF2329	tRNA-pseudouridine
256	4	100.0	231	2	T50827	superoxide dismuta	329	4	100.0	282	2	S73636	hypothetical prote
257	4	100.0	231	2	S62402	major facilitator	330	4	100.0	282	2	AC1177	hypothetical prote
258	4	100.0	231	2	H85138	hypothetical prote	331	4	100.0	282	2	AG1534	hypothetical prote
259	4	100.0	232	2	D75062	probable flagella-	332	4	100.0	282	2	E90526	hypothetical prote
260	4	100.0	232	2	H71169	hypothetical prote	333	4	100.0	283	2	P96616	hypothetical prote
261	4	100.0	232	2	T16315	hypothetical prote	334	4	100.0	283	2	B83618	probable CoA trans
262	4	100.0	233	2	H86666	phosphoglycerate m	335	4	100.0	283	2	B70926	probable viub prot
263	4	100.0	233	2	A25814	glycoprotein 185 -	336	4	100.0	284	2	T29610	hypothetical viub prot
264	4	100.0	233	2	T10198	hypothetical prote	337	4	100.0	285	2	T25971	hypothetical prote
265	4	100.0	233	2	AB1712	hypothetical prote	338	4	100.0	285	2	A97487	probable iron-sulf
266	4	100.0	236	1	R3NT2	ribosomal protein	339	4	100.0	287	2	S55922	TAX responsive ele
267	4	100.0	236	1	R3SF2	ribosomal protein	340	4	100.0	287	2	AC1473	transcription regu
268	4	100.0	236	1	R3PM2	ribosomal protein	341	4	100.0	287	2	AG1111	transcription regu
269	4	100.0	236	1	R3R22	ribosomal protein	342	4	100.0	288	2	S33714	ribosomal protein
270	4	100.0	236	1	R3ZM2	ribosomal protein	343	4	100.0	288	2	I51803	TAXRER107 - human
271	4	100.0	236	1	R3WT2	ribosomal protein	344	4	100.0	289	2	B72099	conserved hypotet
272	4	100.0	237	1	R3EJ2B	ribosomal protein	345	4	100.0	289	2	H86522	CT144 Hypothetical
273	4	100.0	241	2	T00988	hypothetical prote	346	4	100.0	290	2	A11730	Lactobacillus delb
274	4	100.0	243	2	AG3188	hypothetical prote	347	4	100.0	291	2	G81407	hypothetical prote
275	4	100.0	243	2	G98156	hypothetical prote	348	4	100.0	292	2	G72530	probable nicotine
276	4	100.0	244	1	RSBYL7	ribosomal protein	349	4	100.0	292	2	T02737	probable ubiquitin
277	4	100.0	244	2	S55910	probable transpor	350	4	100.0	293	2	T09171	ribosomal protein
278	4	100.0	244	2	A39206	hypothetical prote	351	4	100.0	293	2	T09170	ribosomal protein
279	4	100.0	246	2	T33965	hypothetical prote	352	4	100.0	294	2	A71946	hypothetical prote
280	4	100.0	251	2	E90411	ABC transporter, A	353	4	100.0	293	2	E95234	ABC transporter, A
281	4	100.0	251	2	T39776	60s ribosomal prot	354	4	100.0	294	2	E81420	probable flagellar
282	4	100.0	252	2	T24939	hypothetical prote	355	4	100.0	295	2	AE2367	hypothetical prote
283	4	100.0	252	2	S56325	hiap protein-like	356	4	100.0	297	2	H83309	probable transcrip
284	4	100.0	252	2	E86104	ATP-binding compon	357	4	100.0	297	2	T50782	ribosomal protein
285	4	100.0	252	2	H91263	ATP-binding compon	358	4	100.0	298	2	D69351	hypothetical prote
286	4	100.0	253	2	C70914	probable membrane	359	4	100.0	298	2	F69875	pyrimidine-chlamin
287	4	100.0	253	2	AF2428	hypothetical prote	360	4	100.0	298	2	C97183	probable nucleotid
288	4	100.0	253	2	AG3163	hypothetical prote	361	4	100.0	298	2	T45527	ECM9 homolog (imp
289	4	100.0	253	2	AB3586	integral membrane	362	4	100.0	299	2	H84661	heme oxygenase 2 (
290	4	100.0	254	2	B84901	hypothetical prote	363	4	100.0	300	2	T41066	mitochondrial carr
291	4	100.0	256	2	C89689	trans-2-enoyl-ACP	364	4	100.0	300	2	S58779	probable carrier p
292	4	100.0	258	2	A45161	serine proteinase	365	4	100.0	302	2	P00387	matrix protein - m
293	4	100.0	258	2	F72052	peptidyl-prolyl ci	366	4	100.0	302	2	P00379	matrix protein - m
294	4	100.0	258	2	B86573	FKBP-type peptidyl	367	4	100.0	302	2	P00375	matrix protein - m
295	4	100.0	258	2	G96798	hypothetical prote	368	4	100.0	302	2	P00383	matrix protein - m
296	4	100.0	259	2	B83915	hypothetical prote	369	4	100.0	303	2	H97742	hypothetical prote
297	4	100.0	260	2	B83092	probable cytochrom	370	4	100.0	303	2	B83691	hypothetical prote
298	4	100.0	261	2	G86793	hypothetical prote	371	4	100.0	303	2	T23583	hypothetical prote
299	4	100.0	262	2	AB1196	enoyl - acyl-carrie	372	4	100.0	305	2	E72322	conserved hypotet
300	4	100.0	262	2	AH1553	enoyl - acyl-carrie	373	4	100.0	305	2	S40927	hypothetical prote
301	4	100.0	263	2	AF0420	phosphonates trans	374	4	100.0	305	2	T33578	hypothetical prote
302	4	100.0	264	2	D85097	hypothetical prote	375	4	100.0	306	2	A54717	palmitoyl-protein
303	4	100.0	264	2	B71448	hypothetical prote	376	4	100.0	307	2	C85363	hypothetical prote
304	4	100.0	265	2	H72233	purine nucleoside	377	4	100.0	308	2	T29746	hypothetical prote
305	4	100.0	266	2	C75179	hypothetical prote	378	4	100.0	309	2	T31833	hypothetical prote
306	4	100.0	266	2	G71034	hypothetical prote	379	4	100.0	310	2	T33972	hypothetical prote
307	4	100.0	267	2	D83313	probable permease	380	4	100.0	311	2	F81188	hypothetical prote
308	4	100.0	268	2	C71673	dimethyladenosine	381	4	100.0	311	2	B81990	hypothetical prote
309	4	100.0	269	2	F95106	probable molybdate	382	4	100.0	313	2	C83874	arsenical pump-dri
310	4	100.0	269	2	H97974	Cof family protein	383	4	100.0	313	2	A90097	hypothetical prote
311	4	100.0	269	2	H97974	conserved hypotet	384	4	100.0	314	1	WZBRD7	33.8K capsid prote
312	4	100.0	269	2	T38995	hypothetical prote	385	4	100.0	314	2	T30523	dihydroorotate den
313	4	100.0	270	2	C72073	metal dependent hy	386	4	100.0	315	2	T06053	probable ubiquitin
314	4	100.0	270	2	C86550	metal dependent hy	387	4	100.0	315	2	E71729	probable ubiquitin
315	4	100.0	271	2	G89929	hypothetical prote	388	4	100.0	316	2	T28942	hypothetical prote
316	4	100.0	271	2	A53268	T-cell receptor al	389	4	100.0	316	2	S77783	hypothetical prote
317	4	100.0	271	2	B84861	SOS ribosomal prot	390	4	100.0	317	2	T17792	hypothetical prote
318	4	100.0	271	2	B98007	conserved hypotet	391	4	100.0	318	2	F38688	COI intron 13 prot
319	4	100.0	274	2	AD2548	hypothetical prote	392	4	100.0	319	2	T48504	hypothetical prote
320	4	100.0	279	2	S04693	T-cell receptor de	393	4	100.0	320	2	D70473	phosphate transpor
321	4	100.0	280	2	A42712	formate dehydrogen	394	4	100.0	320	2	T23161	hypothetical prote

395	4	100.0	320	2	C84599	probable ubiquitin	468	4	100.0	359	2	S45700	G-alpha-11 protein
396	4	100.0	321	2	AD1658	probable transmembr	469	4	100.0	360	2	JN0115	GTP-binding regula
397	4	100.0	322	2	A11286	probable transmembr	470	4	100.0	360	2	H71828	probable tRNA (5-m
398	4	100.0	321	2	G72421	iron(III) ABC tran	471	4	100.0	360	2	G64686	conserved hypotet
399	4	100.0	323	2	F89845	hypothetical prote	472	4	100.0	360	2	A72423	D-mannosate hydrol
400	4	100.0	323	2	F83464	flagellar motor sw	473	4	100.0	361	2	E84506	probable N-acetyl
401	4	100.0	323	2	E80297	hypothetical prote	474	4	100.0	362	2	JC7559	sphingosine 1-phos
402	4	100.0	324	2	F95386	protein [imported	475	4	100.0	362	2	C71311	probable phosphat
403	4	100.0	325	1	XYECP4	site-specific DNA-	476	4	100.0	363	2	AF1801	phosphoserine amin
404	4	100.0	326	2	F96522	hypothetical prote	477	4	100.0	363	2	AH1427	phosphoserine amin
405	4	100.0	327	2	T33254	hypothetical prote	478	4	100.0	363	2	H83893	hypothetical prote
406	4	100.0	328	2	T31252	1, 2-dihydroxybenz	479	4	100.0	363	2	D29156	hypothetical prote
407	4	100.0	329	2	S11580	storage protein, b	480	4	100.0	363	2	D83975	hypothetical prote
408	4	100.0	329	2	S17765	major storage prot	481	4	100.0	364	2	T16376	hypothetical prote
409	4	100.0	329	2	D96834	hypothetical prote	482	4	100.0	364	2	T29153	hypothetical prote
410	4	100.0	330	2	G84127	phosphotransactyl	483	4	100.0	365	2	E82585	histidinol-phospha
411	4	100.0	330	2	AF0192	probable C4-dicarb	484	4	100.0	366	1	S35189	dihydrokaempferol
412	4	100.0	330	2	E82936	conserved hypotet	485	4	100.0	366	2	S48110	neurotoxin type F
413	4	100.0	330	2	T26317	hypothetical prote	486	4	100.0	366	2	C82201	spermidine/putresc
414	4	100.0	331	2	T26871	hypothetical prote	487	4	100.0	367	2	D72376	pectate lyase - Th
415	4	100.0	332	2	JC5310	galactose represso	488	4	100.0	370	2	AG0761	probable propanol
416	4	100.0	332	2	H72313	transcription regu	489	4	100.0	370	2	S72195	GTP-binding regula
417	4	100.0	332	2	D90405	geranylgeranyl hyd	490	4	100.0	371	2	AE2162	hypothetical prote
418	4	100.0	332	2	H82084	conserved hypotet	491	4	100.0	372	1	QXVB1	NADH2 dehydrogenas
419	4	100.0	333	2	G87154	GDP-glucose 4,6-d	492	4	100.0	372	2	AG1834	NADH dehydrogenas
420	4	100.0	334	2	C84964	hypothetical prote	493	4	100.0	372	2	A90508	conserved hypotet
421	4	100.0	335	1	MFNZMV	matrix protein - m	494	4	100.0	372	2	T44318	transposase homolo
422	4	100.0	335	1	MFNZMH	matrix protein - m	495	4	100.0	373	1	AJHYQ	glutamate-ammonia
423	4	100.0	335	1	D48556	matrix protein - m	496	4	100.0	373	1	AJRTQ	glutamate-ammonia
424	4	100.0	335	2	AC3367	UDPglucose 4-epime	497	4	100.0	373	2	S41452	glutamate-ammonia
425	4	100.0	335	2	S35933	matrix protein - m	498	4	100.0	373	2	S65176	hypothetical prote
426	4	100.0	335	2	B49601	matrix protein M -	499	4	100.0	374	2	S46810	hypothetical prote
427	4	100.0	335	2	S11227	matrix protein - m	500	4	100.0	376	1	NMBST	exo-alpha-sialidas
428	4	100.0	335	2	S47304	gene M protein - r	501	4	100.0	376	2	T31832	hypothetical prote
429	4	100.0	335	2	T46167	hypothetical prote	502	4	100.0	377	2	B97185	glycosyltransferas
430	4	100.0	335	2	AC0570	FluM protein precu	503	4	100.0	378	2	T40243	hypothetical prote
431	4	100.0	336	2	S22619	hypothetical prote	504	4	100.0	379	2	D96816	hypothetical prote
432	4	100.0	336	2	G87202	probable membrane	505	4	100.0	380	2	T06787	gibberellin 20-oxi
433	4	100.0	338	2	T44844	UDPglucose 4-epime	506	4	100.0	380	2	T06439	gibberellin 20-oxi
434	4	100.0	338	2	D69405	Na+/H+ antiporter	507	4	100.0	380	2	H69427	probable phosphono
435	4	100.0	339	2	A81351	signal transductio	508	4	100.0	380	2	D64352	hypothetical prote
436	4	100.0	342	2	G59502	histidinol-phospha	509	4	100.0	382	2	A10153	conserved hypotet
437	4	100.0	343	1	C70418	probable alcohol d	510	4	100.0	383	2	H75129	probable transamin
438	4	100.0	343	1	MFNZBK	matrix protein - m	511	4	100.0	383	2	H71848	probable na+/h+ an
439	4	100.0	343	2	C69966	hypothetical prote	512	4	100.0	383	2	G64667	probable fatty aci
440	4	100.0	343	2	T07185	hypothetical prote	513	4	100.0	384	1	S54484	probable fatty aci
441	4	100.0	344	2	T05987	hypothetical prote	514	4	100.0	384	2	AE1636	N-acetylornithine
442	4	100.0	344	2	JC5942	chemokine receptor	515	4	100.0	384	2	T26070	hypothetical prote
443	4	100.0	344	2	T33284	hypothetical prote	516	4	100.0	386	2	E71001	probable transamin
444	4	100.0	345	2	AG0366	thiosulfate-bindin	517	4	100.0	386	2	G97316	NADH-dependent but
445	4	100.0	346	2	T11194	NADH2 dehydrogenas	518	4	100.0	387	2	E84664	probable cyclin [i
446	4	100.0	346	2	A82238	histidinol-phospha	519	4	100.0	387	2	S61615	hypothetical prote
447	4	100.0	346	2	T30134	hypothetical prote	520	4	100.0	387	2	H84067	NADH-dependent but
448	4	100.0	346	2	C70105	hypothetical prote	521	4	100.0	388	2	S75920	hypothetical prote
449	4	100.0	346	2	G96643	hypothetical prote	522	4	100.0	388	2	B89777	capsular polysacch
450	4	100.0	347	2	D81288	probable fucose sy	523	4	100.0	389	2	A12230	mannose-1-phosphat
451	4	100.0	347	2	B36018	membrane antigen p	524	4	100.0	389	2	T19883	hypothetical prote
452	4	100.0	347	2	T20618	hypothetical prote	525	4	100.0	391	2	T51737	RNA helicase RH2 [
453	4	100.0	347	2	A82358	hypothetical prote	526	4	100.0	391	2	T13182	integrase - Lactob
454	4	100.0	349	2	E35858	conserved hypotet	527	4	100.0	392	2	E97272	probable membrane-
455	4	100.0	350	2	T10498	UDPglucose 4-epime	528	4	100.0	392	2	B82887	conserved hypotet
456	4	100.0	350	2	S61581	hypothetical prote	529	4	100.0	393	2	S67763	probable membrane
457	4	100.0	351	2	S63197	hypothetical prote	530	4	100.0	395	1	S27363	methionine adenosy
458	4	100.0	352	2	T07229	photosystem II pro	531	4	100.0	395	2	D81146	aminotransferase,
459	4	100.0	352	2	G71328	probable flagellar	532	4	100.0	395	2	B81877	probable aminotran
460	4	100.0	352	2	T48903	wax synthase [impo	533	4	100.0	396	2	A47151	methionine adenosy
461	4	100.0	353	2	E84941	imidazoleglycerol-	534	4	100.0	397	2	S06114	methionine adenosy
462	4	100.0	355	2	E36785	protein F10A5.28 [	535	4	100.0	397	2	S42039	hypothetical prote
463	4	100.0	357	2	G70577	probable dihydroor	536	4	100.0	401	2	AG0172	probable nicotinac
464	4	100.0	357	2	A88969	protein T27B7.7 [i	537	4	100.0	401	2	D64500	glucose-6-phosphat
465	4	100.0	358	1	S74846	hypothetical prote	538	4	100.0	401	2	F90810	flagellar hook pro
466	4	100.0	358	2	S19993	acid phosphatase (	539	4	100.0	401	2	B85670	flagellar biosynth
467	4	100.0	358	2	T31490	hypothetical prote	540	4	100.0	404	2	B41317	O-antigen ligase c

541	4	100.0	404	2	AE0973	O-antigen ligase l	614	4	100.0	449	2	G85332	hypothetical prote
542	4	100.0	404	2	G72385	conserved hypothet	615	4	100.0	449	2	T10650	hypothetical prote
543	4	100.0	405	2	A72383	sensor histidine k	616	4	100.0	450	2	E95257	hypothetical prote
544	4	100.0	406	2	B81391	zinc proteinase-11	617	4	100.0	450	2	E98122	replicative DNA he
545	4	100.0	407	2	E98347	hypothetical prote	618	4	100.0	450	2	A72015	conserved hypothet
546	4	100.0	408	2	AB2935	conserved hypothet	619	4	100.0	450	2	B86610	CT805 hypothetical
547	4	100.0	409	2	T29857	probable aspartate	620	4	100.0	450	2	T37628	glycerol dehydroge
548	4	100.0	409	2	H90096	eukaryotic release	621	4	100.0	451	2	S33612	isocitrate dehydro
549	4	100.0	409	2	S24460	probable membrane	622	4	100.0	453	2	H86882	DNA repair protein
550	4	100.0	410	2	T25574	hypothetical prote	623	4	100.0	453	2	S57140	probable membrane
551	4	100.0	411	2	E97088	sugar-proton sympo	624	4	100.0	454	2	A46498	glucocorticoid-sen
552	4	100.0	411	2	A44121	ribosomal protein	625	4	100.0	456	2	S16291	phosphomannomutase
553	4	100.0	412	2	S28423	isocitrate dehydro	626	4	100.0	456	2	AE0768	hypothetical prote
554	4	100.0	412	2	A72290	conserved hypothet	627	4	100.0	457	2	D96735	hypothetical prote
555	4	100.0	415	2	S65065	isocitrate dehydro	628	4	100.0	457	2	H86193	hypothetical prote
556	4	100.0	416	2	S47013	isocitrate dehydro	629	4	100.0	458	2	T16041	hypothetical prote
557	4	100.0	416	2	A96585	NADP specific isoc	630	4	100.0	458	2	F86433	protein T17H7.5 [l
558	4	100.0	416	2	H69252	alcohol dehydrogen	631	4	100.0	460	2	A10078	hypothetical prote
559	4	100.0	416	2	S44063	phosphoglycerate k	632	4	100.0	461	2	S72953	probable GTP-bindl
560	4	100.0	416	2	S43279	cell division cont	633	4	100.0	461	2	H90090	hypothetical prote
561	4	100.0	416	2	F71869	hypothetical prote	634	4	100.0	461	2	T48015	hypothetical prote
562	4	100.0	416	2	T47173	hypothetical prote	635	4	100.0	462	2	F87080	probable GMP-bindl
563	4	100.0	417	2	S68151	phosphoglycerate k	636	4	100.0	466	2	PC4296	nicotinic acetylch
564	4	100.0	417	2	S00933	DNA-directed RNA p	637	4	100.0	468	2	S46179	regulatory protein
565	4	100.0	417	2	F70132	conserved hypothet	638	4	100.0	468	2	S47447	hypothetical prote
566	4	100.0	417	2	S25627	glucose-1-phosphat	639	4	100.0	469	2	T17191	dihydroliipoamide d
567	4	100.0	418	2	E71716	proline/betaine tr	640	4	100.0	469	2	E95236	glycosyl hydrolase
568	4	100.0	418	2	C97713	proline/betaine tr	641	4	100.0	470	2	A39218	nicotinic acetylch
569	4	100.0	420	2	T32426	hypothetical prote	642	4	100.0	471	2	F64213	hypothetical prote
570	4	100.0	420	2	C87790	protein B0207.3 [l	643	4	100.0	472	1	S55379	cytochrome P450 Cy
571	4	100.0	420	2	H96534	probable Na+/H+ an	644	4	100.0	475	2	B90545	atp synthase beta
572	4	100.0	421	1	S70433	zona pellucida gly	645	4	100.0	475	2	AB3473	uroporphyrin-III C
573	4	100.0	421	1	S70402	zona pellucida gly	646	4	100.0	476	2	C81351	probable UDP-N-ac
574	4	100.0	421	1	D86596	CLP proteinase ATP	647	4	100.0	476	2	A41463	alkaline metallopr
575	4	100.0	421	1	F72028	ATP-dependent Clp	648	4	100.0	476	2	A43942	lipase Pseudomon
576	4	100.0	422	1	A60503	sperm-binding gly	649	4	100.0	477	1	A64211	Pert12 protein hom
577	4	100.0	422	2	T45830	hypothetical prote	650	4	100.0	477	2	S48045	toxlin apxIII secre
578	4	100.0	422	2	AH1129	a module of peptid	651	4	100.0	478	2	S21454	glutamate-1-semial
579	4	100.0	423	2	T15309	hypothetical prote	652	4	100.0	478	2	S21455	nadh oxidase (noxa
580	4	100.0	424	2	T44296	hypothetical prote	653	4	100.0	478	2	G90514	alkaline metallopr
581	4	100.0	426	2	E70368	histidinol dehydro	654	4	100.0	479	1	S26699	NADH2 dehydrogenas
582	4	100.0	426	2	S70396	zona pellucida gly	655	4	100.0	479	2	C95366	probable phosphodi
583	4	100.0	428	2	T48008	hypothetical prote	656	4	100.0	479	2	T03293	lipopolysaccharide
584	4	100.0	428	2	G89982	hypothetical prote	657	4	100.0	479	2	D72354	probable cytochrom
585	4	100.0	430	2	AF3558	sarcosine oxidase	658	4	100.0	481	2	B96691	altronate oxidore
586	4	100.0	430	2	T27152	hypothetical prote	659	4	100.0	482	2	E96985	beta-glucosidase (
587	4	100.0	430	2	G70487	sulfide-quinone re	660	4	100.0	483	2	G98100	hypothetical prote
588	4	100.0	432	2	H64514	hypothetical prote	661	4	100.0	484	2	T33504	hypothetical prote
589	4	100.0	432	2	A69056	hypothetical prote	662	4	100.0	486	2	T23405	hypothetical prote
590	4	100.0	433	2	T09619	isocitrate dehydro	663	4	100.0	487	2	T32341	hypothetical prote
591	4	100.0	433	2	T17654	hypothetical prote	664	4	100.0	488	2	T51502	hypothetical prote
592	4	100.0	435	2	AE1269	glutamyl-tRNA redu	665	4	100.0	488	2	E81403	hypothetical prote
593	4	100.0	435	2	AG1631	glutamyl-tRNA redu	666	4	100.0	490	2	T43184	DEAD box ATP-depen
594	4	100.0	435	2	G69779	atserical pump mem	667	4	100.0	490	2	A96745	probable cytosolic
595	4	100.0	436	2	A13381	seleuocysteine lya	668	4	100.0	491	2	B70414	NADH2 dehydrogenas
596	4	100.0	437	2	F70114	probable zinc prot	669	4	100.0	491	2	I40455	penicillin binding
597	4	100.0	438	2	T07402	probable isocitrat	670	4	100.0	491	2	A70681	probable dectA prot
598	4	100.0	440	2	AE0171	probable killing f	671	4	100.0	492	2	T01584	cellulase (EC 3.2.
599	4	100.0	441	2	SS4734	translation elonga	672	4	100.0	493	2	G90604	hypothetical prote
600	4	100.0	441	2	AB1367	aminopeptidase C l	673	4	100.0	495	1	FW8Y2	glycinn chain Ala
601	4	100.0	441	2	AC1736	signal recognition	674	4	100.0	495	2	S10851	glycinn Gl precu
602	4	100.0	442	2	F69042	chiophene and fura	675	4	100.0	497	2	T32090	hypothetical prote
603	4	100.0	442	2	E90513	anthranilate N-hyd	676	4	100.0	498	2	G96938	senory transducti
604	4	100.0	443	2	AG0428	hypothetical 48.8	677	4	100.0	499	2	AH2413	alginate o-acetyl
605	4	100.0	443	2	T45574	hypothetical 48.8	678	4	100.0	499	2	G82923	multiple banded an
606	4	100.0	445	1	D65171	D-alanine/glycine	679	4	100.0	500	2	S16788	probable reverse t
607	4	100.0	445	1	A45111	hydroxyproline-ric	680	4	100.0	500	2	H91283	hypothetical prote
608	4	100.0	446	2	T07907	hypothetical prote	681	4	100.0	500	2	T39385	probable mitochond
609	4	100.0	447	2	F90248	hypothetical prote	682	4	100.0	500	2	B86125	hypothetical prote
610	4	100.0	447	2	T25264	NADH oxidase (noxa	683	4	100.0	502	2	S56489	hypothetical 54.3K
611	4	100.0	448	2	A69482	hypothetical prote	684	4	100.0	502	2	B90103	T-complex protein
612	4	100.0	448	2	D90741	hypothetical prote	685	4	100.0	503	2	C82068	aminopeptidase A/I
613	4	100.0	448	2	SS7147	probable membrane	686	4	100.0	506	2	T23576	hypothetical prote

687	4	100.0	506	2	JC5678	minor core protein	760	4	100.0	599	2	G85591	probable pyruvate
688	4	100.0	507	1	A30828	steroid 17alpha-mo	761	4	100.0	601	2	T02633	hypothetical prote
689	4	100.0	508	1	A39072	steroid 17alpha-mo	762	4	100.0	602	2	G75278	DEAD box ATP-depen
690	4	100.0	509	2	T48459	cytochrome P450-11	763	4	100.0	604	2	T41249	hypothetical prote
691	4	100.0	509	2	T48168	hypothetical prote	764	4	100.0	605	2	C90111	hypothetical prote
692	4	100.0	509	2	C95900	probable sugar ABC	765	4	100.0	606	2	H97012	protein T16Al.1 li
693	4	100.0	513	2	AE0021	conserved hypothet	766	4	100.0	607	2	H88065	hypothetical prote
694	4	100.0	516	2	A87260	conserved hypothet	767	4	100.0	607	2	G60905	Gcpg protein limpo
695	4	100.0	518	2	AE3553	serine-type D-Ala-	768	4	100.0	613	2	C86537	triacylglycerol li
696	4	100.0	518	2	S55948	hypothetical prote	769	4	100.0	613	2	JS0763	gcpE protein CP038
697	4	100.0	519	2	A26334	2-isopropylmalate	770	4	100.0	613	2	E72087	hypothetical prote
698	4	100.0	519	2	C90085	hypothetical prote	771	4	100.0	615	2	B85713	hypothetical prote
699	4	100.0	520	1	A42209	D-sterespecific a	772	4	100.0	616	2	A95969	anaerobic ribonuel
700	4	100.0	522	2	H72267	conserved hypothet	773	4	100.0	618	2	E72285	ABC transporter, p
701	4	100.0	522	2	E86365	protein F3F19.15 l	774	4	100.0	618	2	S68513	thyroid iodide tra
702	4	100.0	526	2	AB3433	C-di-GMP phosphodi	775	4	100.0	621	2	A75101	aldehyde-ferredoxi
703	4	100.0	530	2	B87369	long-chain-fatty-a	776	4	100.0	622	2	D44986	apical membrane an
704	4	100.0	530	2	D70218	oligopeptide ABC t	777	4	100.0	622	2	B44986	apical membrane an
705	4	100.0	533	2	F70551	hypothetical prote	778	4	100.0	622	2	A32499	apical membrane an
706	4	100.0	534	2	T50067	probable tRNA nucl	779	4	100.0	622	2	A44986	apical membrane an
707	4	100.0	535	2	A60531	probable esterase	780	4	100.0	622	2	C44986	apical membrane an
708	4	100.0	538	2	AD0285	probable periplasm	781	4	100.0	624	2	H90071	hypothetical prote
709	4	100.0	539	1	A42467	alkaline phosphata	782	4	100.0	627	2	G86860	serine/threonine p
710	4	100.0	540	2	F86745	ABC transporter pe	783	4	100.0	627	2	T00124	hypothetical prote
711	4	100.0	540	2	T48619	tRNA synthase-like	784	4	100.0	629	2	T22848	hypothetical prote
712	4	100.0	541	2	F86806	lipopolysaccharide	785	4	100.0	629	2	AE2497	hypothetical prote
713	4	100.0	542	2	S60616	capsid protein - h	786	4	100.0	630	2	JQ1894	hypothetical prote
714	4	100.0	544	2	E75569	probable aminotran	787	4	100.0	632	2	T38126	hypothetical 74.lk
715	4	100.0	545	2	T00453	probable AMP-bindi	788	4	100.0	633	2	H95932	probable electron
716	4	100.0	545	2	F64579	site-specific DNA-	789	4	100.0	638	2	S54418	probable adenyl-
717	4	100.0	545	2	F71932	type II DNA modifi	790	4	100.0	640	2	E88575	fibronectin-bindin
718	4	100.0	545	2	F95325	probable arylsulfa	791	4	100.0	640	2	E90590	protein ZK128.6 l
719	4	100.0	547	2	H75632	Na(+)-linked D-ala	792	4	100.0	641	1	ZZZRNQ	hypothetical prote
720	4	100.0	547	2	AF3302	hypothetical prote	793	4	100.0	641	2	E95320	adenyl-lyl-sulfate k
721	4	100.0	548	2	C70253	adenine deaminase	794	4	100.0	642	2	S37623	hypothetical prote
722	4	100.0	550	2	C86348	probable amp-bindi	795	4	100.0	645	2	T25824	hypothetical prote
723	4	100.0	551	2	F69282	medium-chain acyl-	796	4	100.0	646	1	S16654	RNA-directed DNA p
724	4	100.0	551	2	T00932	hypothetical prote	797	4	100.0	647	2	T28214	probable nucleosid
725	4	100.0	552	2	T07932	probable amp-bindi	798	4	100.0	647	2	E82126	DNA topoisomerase
726	4	100.0	554	2	T25902	hypothetical prote	799	4	100.0	649	1	TVVPMK	large T antigen -
727	4	100.0	554	2	S59235	hypothetical prote	800	4	100.0	650	2	A70817	probable fadE10 pr
728	4	100.0	555	2	AC0585	glutamyl-tRNA sy	801	4	100.0	650	2	T32897	hypothetical prote
729	4	100.0	555	2	AC2467	hypothetical prote	802	4	100.0	652	2	T16582	hypothetical prote
730	4	100.0	557	2	H96590	hypothetical prote	803	4	100.0	653	2	A49722	endoglin precursor
731	4	100.0	558	2	T19748	hypothetical prote	804	4	100.0	655	2	G96524	protein T1N15.9 l
732	4	100.0	558	2	C96933	2-isopropylmalate	805	4	100.0	655	2	H71420	hypothetical prote
733	4	100.0	560	2	S23313	hypothetical prote	806	4	100.0	657	2	E90254	formate dehydrogen
734	4	100.0	562	2	G87005	probable two-compo	807	4	100.0	658	2	B84664	probable receptor-
735	4	100.0	564	2	A86145	hypothetical prote	808	4	100.0	659	2	S40043	adhesin - Streptoc
736	4	100.0	565	2	A25226	RAD7 protein - Yea	809	4	100.0	661	2	T08314	hypothetical prote
737	4	100.0	566	2	T06724	protein disulfide-	810	4	100.0	662	2	E84725	ankyrin-like prote
738	4	100.0	566	2	F84903	probable ubiquitin	811	4	100.0	664	1	S73624	hypothetical prote
739	4	100.0	567	2	C69611	ABC transporter re	812	4	100.0	664	2	D96633	hypothetical prote
740	4	100.0	567	2	G70552	probable mtrB prot	813	4	100.0	665	2	D90092	hypothetical prote
741	4	100.0	569	2	T43531	probable potassium	814	4	100.0	666	2	T08904	probable long-chai
742	4	100.0	570	2	T46011	hypothetical prote	815	4	100.0	666	2	T08182	probable long-chai
743	4	100.0	570	2	G88098	protein F18A12.3 l	816	4	100.0	667	1	E64240	hypothetical prote
744	4	100.0	572	2	T16780	hypothetical prote	817	4	100.0	667	2	T07929	probable long-chai
745	4	100.0	573	1	C64131	acetylactate synth	818	4	100.0	667	2	E84018	two-component sens
746	4	100.0	573	1	A53651	sulfate adenyl-lytr	819	4	100.0	669	2	A49585	Na+ channel protei
747	4	100.0	574	1	S55034	sulfate adenyl-lytr	820	4	100.0	670	2	T33304	hypothetical prote
748	4	100.0	574	2	T16328	hypothetical prote	821	4	100.0	680	2	T27699	hypothetical prote
749	4	100.0	576	2	A71497	probable DNA misma	822	4	100.0	680	2	T27078	hypothetical prote
750	4	100.0	576	2	E70539	probable membranep	823	4	100.0	681	2	B72009	conserved hypothet
751	4	100.0	576	2	T16005	hypothetical prote	824	4	100.0	681	2	G86614	CT837 hypothetical
752	4	100.0	578	2	H82402	methyl-accepting c	825	4	100.0	683	2	JE0262	long-chain-fatty-a
753	4	100.0	584	2	S49594	capsid protein VP2	826	4	100.0	683	2	A57037	dynamin intermediat
754	4	100.0	586	1	RNEGB1	DNA-directed RNA p	827	4	100.0	683	2	E86358	Fl2K8.13 protein -
755	4	100.0	589	2	S64372	probable membrane	828	4	100.0	684	2	S41788	endo-1,4-beta-xyla
756	4	100.0	591	2	D64204	membrane lipoprote	829	4	100.0	686	2	T23721	hypothetical prote
757	4	100.0	594	2	B69132	translational initia	830	4	100.0	687	1	XUVKG	UDPglucose 4-epime
758	4	100.0	596	2	F81251	NADH2 dehydrogenas	831	4	100.0	687	2	T02459	probable beta-amyl
759	4	100.0	596	2	T03908	hypothetical prote	832	4	100.0	689	2	E75141	cation-transportin

833	4	100.0	689	2	T40364	hypothetical prote	906	4	100.0	794	2	T09643	glutamine-tRNA lig
834	4	100.0	690	2	S54211	ATM1 protein precu	907	4	100.0	794	2	D84765	similar to mammali
835	4	100.0	691	2	T41724	Probabl adenosine	908	4	100.0	795	2	AC0129	probable surface a
836	4	100.0	692	1	G97400	sensor/response re	909	4	100.0	802	2	AC2075	outer membrane hem
837	4	100.0	693	1	A49795	Alzheimer's diseas	910	4	100.0	803	2	B84931	DNA topoisomerase
838	4	100.0	695	2	A27485	Alzheimer's diseas	911	4	100.0	803	2	AB0530	outer membrane pro
839	4	100.0	695	2	S00550	Alzheimer's diseas	912	4	100.0	808	1	T16564	hypothetical prote
840	4	100.0	696	2	T21109	hypothetical prote	913	4	100.0	810	1	G64819	probable formate C
841	4	100.0	696	2	T11674	glutamine-fructose	914	4	100.0	810	2	AG0602	formate C-acetyltr
842	4	100.0	699	2	C97176	cation transport p	915	4	100.0	810	2	A64742	hypothetical prote
843	4	100.0	699	2	S29499	sodium channel pro	916	4	100.0	810	2	C90651	hypothetical prote
844	4	100.0	700	2	D90926	hypothetical prote	917	4	100.0	810	2	C85502	hypothetical prote
845	4	100.0	700	2	H85774	hypothetical prote	918	4	100.0	812	2	E95029	formate acetyltran
846	4	100.0	700	2	A64925	probable oxidoredu	919	4	100.0	812	2	A83379	glycogen phosphory
847	4	100.0	702	2	G96608	hypothetical prote	920	4	100.0	815	2	H97900	formate C-acetyltr
848	4	100.0	705	1	C1HURB	complement subcomp	921	4	100.0	815	2	T09450	hypothetical prote
849	4	100.0	705	1	T12784	sublancin 168 lanc	922	4	100.0	820	2	A86510	hypothetical prote
850	4	100.0	705	2	F82534	translacton elonga	923	4	100.0	820	2	C72113	leucine-tRNA synthe
851	4	100.0	705	2	B82885	hypothetical prote	924	4	100.0	825	2	H82885	hypothetical prote
852	4	100.0	705	2	T01730	hypothetical prote	925	4	100.0	830	2	S50810	probable membrane
853	4	100.0	706	2	D82452	anaerobic ribonuc	926	4	100.0	835	2	F70363	cation transportin
854	4	100.0	707	1	A64047	ribonucleoside-tri	927	4	100.0	836	1	QOVZRA	mRNA guanlyltrans
855	4	100.0	708	2	T00205	hypothetical prote	928	4	100.0	837	2	F90191	integral membrane
856	4	100.0	710	2	AH1109	anaerobic ribonuc	929	4	100.0	838	2	S61250	DNA helicase/prima
857	4	100.0	710	2	T41586	hypothetical serin	930	4	100.0	842	2	T23715	hypothetical prote
858	4	100.0	711	1	TFHUL	lactotransferrin p	931	4	100.0	842	2	T52396	formin-binding pro
859	4	100.0	712	1	A47331	ribonucleoside-tri	932	4	100.0	845	2	T07039	Hcr9-0 protein - t
860	4	100.0	712	2	G86131	anaerobic ribonuc	933	4	100.0	853	2	T17461	disease resistance
861	4	100.0	712	2	G91280	ribonucleoside-tri	934	4	100.0	855	2	T17460	disease resistance
862	4	100.0	712	2	AC1058	hypothetical prote	935	4	100.0	860	2	T27084	hypothetical prote
863	4	100.0	712	2	AG0419	hypothetical prote	936	4	100.0	861	2	D82814	ATP-dependent Clp
864	4	100.0	713	2	G84586	hypothetical prote	937	4	100.0	863	2	H84490	hypothetical prote
865	4	100.0	714	2	C1HMH	calpain (EC 3.4.22	938	4	100.0	863	2	A55173	cf-9 protein precu
866	4	100.0	714	2	D85014	hypothetical prote	939	4	100.0	864	2	C82019	DNA mismatch repa
867	4	100.0	716	2	AB1471	anaerobic ribonuc	940	4	100.0	864	2	AB1000	DNA mismatch repa
868	4	100.0	716	2	T21516	hypothetical prote	941	4	100.0	868	2	S64747	probable membrane
869	4	100.0	716	2	D89837	hypothetical prote	942	4	100.0	872	1	S53319	acetaldehyde dehyd
870	4	100.0	721	1	T40317	actin-like protein	943	4	100.0	881	1	JDVLS	DNA-directed DNA p
871	4	100.0	722	1	VCPVCN	coat protein Vp1 -	944	4	100.0	882	1	WMBEUS	gene ULS protein -
872	4	100.0	722	1	VCPVME	coat protein Vp1 -	945	4	100.0	882	2	A42855	N-heparan sulfate
873	4	100.0	723	2	H85092	hypothetical prote	946	4	100.0	882	2	A57169	[heparan sulfate] -
874	4	100.0	723	2	A41258	a-actinin core	947	4	100.0	883	2	B95237	alcohol dehydrogen
875	4	100.0	726	2	T15810	hypothetical prote	948	4	100.0	883	2	A49733	[heparan sulfate] -
876	4	100.0	727	1	VCPVIF	coat protein Vp1 -	949	4	100.0	888	2	A38539	p101 protein precu
877	4	100.0	727	1	VCPVFP	coat protein Vp1 -	950	4	100.0	891	2	C89101	alcohol-acetaldehy
878	4	100.0	729	2	D86183	probable glutaminy	951	4	100.0	891	2	G89957	hypothetical prote
879	4	100.0	730	2	A46265	P640 (phocovscem	952	4	100.0	896	2	T24169	hypothetical prote
880	4	100.0	733	2	T01875	probable long-chain	953	4	100.0	897	2	T06540	polysynucleotide
881	4	100.0	734	2	F88098	protein F18A12.4 l	954	4	100.0	899	2	T40199	Ca2+-transporting
882	4	100.0	735	2	C86163	hypothetical prote	955	4	100.0	902	2	S26002	gene coxi intrein 1
883	4	100.0	737	1	VCPVCD	coat protein Vp1 -	956	4	100.0	904	1	RGBYPI	regulatory protein
884	4	100.0	745	2	B84673	hypothetical prote	957	4	100.0	906	1	RNBPX1	DNA-directed RNA p
885	4	100.0	746	2	AG2618	hypothetical prote	958	4	100.0	906	2	T24166	hypothetical prote
886	4	100.0	747	2	UH0773	Alzheimer's diseas	959	4	100.0	906	2	T15683	hypothetical prote
887	4	100.0	748	2	VCPVCP	coat protein Vp1 -	960	4	100.0	927	2	A45039	CTF4 protein - yea
888	4	100.0	748	2	D64585	cag pathogenicity	961	4	100.0	932	2	S62555	protoplast regene
889	4	100.0	748	2	F71927	cag island protein	962	4	100.0	933	2	C83514	probable NADH dehy
890	4	100.0	759	2	T00875	hypothetical prote	963	4	100.0	939	2	S55965	probable membrane
891	4	100.0	768	2	B72397	5-methyltetrahydro	964	4	100.0	939	2	H84783	probable PHD-type
892	4	100.0	769	1	D81828	GTP pyrophosphokin	965	4	100.0	965	2	T38430	hypothetical prote
893	4	100.0	770	1	QRHUNA	Alzheimer's diseas	966	4	100.0	966	2	S26235	phosphoenolpyruvat
894	4	100.0	773	1	F90537	glutoprotein limpor	967	4	100.0	967	2	T20336	hypothetical prote
895	4	100.0	775	1	I37432	glutamine-tRNA lig	968	4	100.0	968	2	G90636	hypothetical prote
896	4	100.0	776	2	S59790	hypothetical prote	969	4	100.0	968	2	S46992	probable ATP-depen
897	4	100.0	778	2	C70412	outer membrane pro	970	4	100.0	968	2	G85487	protein p130 - rat
898	4	100.0	779	2	S64680	exoribonuclease 10	971	4	100.0	968	2	AD0514	probable ATP-depen
899	4	100.0	779	2	E71825	probable type III	972	4	100.0	968	2	C64727	probable ATP-depen
900	4	100.0	780	2	D75361	phosphoenolpyruvat	973	4	100.0	970	2	D59435	Gem-interacting pr
901	4	100.0	780	2	AB1801	amino-terminal dom	974	4	100.0	976	2	H97269	Zn-dependent pepti
902	4	100.0	780	2	AC1437	transcription regu	975	4	100.0	977	2	AC1963	DNA polymerase I
903	4	100.0	784	2	AI0513	organic solvent to	976	4	100.0	978	2	H86319	hypothetical prote
904	4	100.0	787	1	S63364	p-aminobenzoate by	977	4	100.0	980	2	S71090	peroxisome biogene
905	4	100.0	787	2	H90543	conserved hypochet	978	4	100.0	984	2	S67609	probable membrane

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979      4 100.0 987 2 A88746
980      4 100.0 1004 2 T31665
981      4 100.0 1008 2 C84679
982      4 100.0 1010 2 T33372
983      4 100.0 1011 2 T07712
984      4 100.0 1012 2 T00958
985      4 100.0 1015 2 T13062
986      4 100.0 1016 2 S30236
987      4 100.0 1017 2 T42384
988      4 100.0 1018 2 A69329
989      4 100.0 1019 2 A38738
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994      4 100.0 1031 2 G96634
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996      4 100.0 1037 2 T18365
997      4 100.0 1037 2 T18368
998      4 100.0 1053 2 T09645
999      4 100.0 1058 2 T13286
1000     4 100.0 1060 2 S06286

protein C18F3.2 [i
hypothetical prote
hypothetical prote
hypothetical prote
probable ABC-type
hypothetical prote
CLOCK protein - fr
genome polyprotein
inositol-1,4,5-tri
probable isoleucin
coagulation factor
CLOCK protein - fr
CLOCK protein - fr
unknown protein F9
hypothetical prote
probable DNA helic
probable calcium-t
polysialyltransfer
polysialyltransfer
DNA-directed RNA p
cappuccino gene pr
major merozoite su

ALIGNMENTS

RESULT 1
F41299
T-cell receptor alpha chain precursor J region (37) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
C:Accession: F41299
R;Umatsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.;
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A>Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatoid
A:Reference number: A41299; MUID:92020887; PMID:1656449
A:Accession: F41299
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <UEM>
A:Cross-references: GB:857448; NID:9236328; PIDN:AAB19961.1; PID:9236329
C:Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 3 KLVP 6

RESULT 2
G32502
T-cell receptor delta chain MLC6, spleen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C:Accession: G32502
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A>Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A:Reference number: A31461; MUID:89128840; PMID:2783779
A:Accession: G32502
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-26 <LAC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 3 KLVP 6

protein C18F3.2 [i
hypothetical prote
hypothetical prote
hypothetical prote
probable ABC-type
hypothetical prote
CLOCK protein - fr
genome polyprotein
inositol-1,4,5-tri
probable isoleucin
coagulation factor
CLOCK protein - fr
CLOCK protein - fr
unknown protein F9
hypothetical prote
probable DNA helic
probable calcium-t
polysialyltransfer
polysialyltransfer
DNA-directed RNA p
cappuccino gene pr
major merozoite su

```

```

Qy 1 KLVP 4
Db 13 KLVP 16

```

## RESULT 3

```

C47719
T-cell receptor alpha chain (V-J region, CD4+ clone DD11, house-dust-mite-reactive) - hu
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: C47719
R;Wedderburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993
A>Title: In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell
A:Reference number: A47719; MUID:93376774; PMID:8367485
A:Accession: C47719
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-29 <WED>
A>Note: sequence extracted from NCBI backbone (NCBIN:137814, NCBI:137820)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

```

```

Query Match 100.0%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KLVP 4
Db 12 KLVP 15

```

## RESULT 4

```

E31461
T-cell receptor delta chain BDN9, thymus - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C:Accession: E31461
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A>Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A:Reference number: A31461; MUID:89128840; PMID:2783779
A:Accession: E31461
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-30 <LAC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

```

```

Query Match 100.0%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 KLVP 4
Db 17 KLVP 20

```

## RESULT 5

```

F31461
T-cell receptor delta chain BDN10, thymus - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C:Accession: F31461
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A>Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A:Reference number: A31461; MUID:89128840; PMID:2783779
A:Accession: F31461
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-31 <LAC>

```

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 18 KLVF 21

RESULT 6

D32502  
T-cell receptor delta chain CDN35, thymus - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: D32502

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: D32502

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-32 <LAC>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 19 KLVF 22

RESULT 7

A32502  
T-cell receptor delta chain CDN26, thymus - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: A32502

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: A32502

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-32 <LAC>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 19 KLVF 22

RESULT 8

D31461  
T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: D31461

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: D31461

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-32 <LAC>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 19 KLVF 22

RESULT 9

B32540  
T-cell receptor delta chain, VDJ region (clone MLC24) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: B32540; B32502

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: B32540

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

A/Experimental source: clone MLC24 (spleen)

A/Accession: B32502

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 20 KLVF 23

RESULT 10

E32502  
T-cell receptor delta chain MLC2, spleen - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C/Accession: E32502

R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A/Reference number: A31461; PMID:89128840; PMID:2783779

A/Accession: E32502

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-33 <LAC>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 20 KLVF 23

```
RESULT 11
I31461
T-cell receptor delta chain CDN15, thymus - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C;Accession: I31461
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A;Reference number: A31461; MUID:89128840; PMID:2783779
A;Accession: I31461
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-33 <LAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 20 KLVF 23

RESULT 12
A31461
T-cell receptor delta chain BDN1, thymus - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C;Accession: A31461
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A;Reference number: A31461; MUID:89128840; PMID:2783779
A;Accession: A31461
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-33 <LAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 20 KLVF 23

RESULT 13
B31461
T-cell receptor delta chain BDN3, thymus - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C;Accession: B31461
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A;Reference number: A31461; MUID:89128840; PMID:2783779
A;Accession: B31461
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-33 <LAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 20 KLVF 23
```

```
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 20 KLVF 23

RESULT 14
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 100.0%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 21 KLVF 24

RESULT 15
I32502
T-cell receptor delta chain MLC17, spleen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C;Accession: I32502
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A;Reference number: A31461; MUID:89128840; PMID:2783779
A;Accession: I32502
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-34 <LAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
   |||
Db 21 KLVF 24

RESULT 16
C31461
T-cell receptor delta chain BDN5, thymus - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997
C;Accession: C31461
R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989
A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.
A;Reference number: A31461; MUID:89128840; PMID:2783779
A;Accession: C31461
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-34 <LAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
```



Query Match 100.0%; Score 4; DB 2; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 21 KLVF 24

## RESULT 17

H31461  
 T-cell receptor delta chain CDN1, thymus - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997  
 C/Accession: H31461  
 R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989  
 A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.  
 A/Reference number: A31461; PMID:89128840; PMID:2783779  
 A/Accession: H31461  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-34 <LAC>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 21 KLVF 24

## RESULT 18

H32502  
 T-cell receptor delta chain MLC13, spleen - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997  
 C/Accession: H32502  
 R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989  
 A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.  
 A/Reference number: A31461; PMID:89128840; PMID:2783779  
 A/Accession: H32502  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-36 <LAC>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 23 KLVF 26

## RESULT 19

A32540  
 T-cell receptor delta chain MLC20, spleen - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997  
 C/Accession: A32540  
 R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989  
 A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.  
 A/Reference number: A31461; PMID:89128840; PMID:2783779  
 A/Accession: A32540

A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-36 <LAC>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 23 KLVF 26

## RESULT 20

C32502  
 T-cell receptor delta chain CDN29, thymus - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997  
 C/Accession: C32502  
 R/Lacy, M.J.; McNeill, L.K.; Roth, M.E.; Kranz, D.M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989  
 A/Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.  
 A/Reference number: A31461; PMID:89128840; PMID:2783779  
 A/Accession: C32502  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-36 <LAC>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 23 KLVF 26

## RESULT 21

PN0512  
 beta-amyloid protein - guinea pig (fragment)  
 C/Species: Cavia porcellus (guinea pig)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C/Accession: PN0512  
 R/Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, I.  
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
 A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragm.  
 A/Reference number: PN0512; PMID:93290653; PMID:7685598  
 A/Accession: PN0512  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: protein  
 A/Residues: 1-42 <SH1>  
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 100.0%; Score 4; DB 2; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 16 KLVF 19

## RESULT 22

PC4133  
 hypothetical 47 protein - Pyrococcus sp. (fragment)  
 C/Species: Pyrococcus sp.  
 C/Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jul-2000  
 C/Accession: PC4133  
 R/Bouyoub, A.; Barbier, G.; Querellou, J.; Forterre, P.

Gene 167, 147-149, 1995

A;Title: A putative SOS repair gene (dinF-like) in a hyperthermophilic archaeon.

A;Reference number: J04561; MUID:96144265; PMID:8566767

A;Accession: PC4133

A;Molecule type: DNA

A;Residues: 1-47 <BOU>

A;Cross-references: EMBL:X91006; NID:g971569; PIDN:CAA62486.1; PID:g971570

A;Experimental source: AL585

Query Match 100.0%; Score 4; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 6 KLVP 9

RESULT 23

PS0009

glycinin AlaBib precursor - soybean (fragments)

C;Species: Glycine max (soybean)

C;Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 15-Nov-1996

C;Accession: PS0009

R;Utsumi, S.; Kim, C.S.; Sato, T.; Kito, M.

Gene 71, 349-358, 1988

A;Title: Signal sequence of preproglycinin affects production of the expressed protein

A;Reference number: PS0009; MUID:93138011; PMID:3066702

A;Accession: PS0009

A;Molecule type: mRNA

A;Residues: 1-53 <UTS>

A;Comment: This protein is composed of six subunits. Each subunit consists of an acidic

C;Superfamily: glycinin

C;Keywords: seed; storage protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-37/Product: glycinin Ala chain (fragment) #status predicted <PEA>

F;38-53/Product: glycinin Bib chain (fragment) #status predicted <PEB>

Query Match 100.0%; Score 4; DB 2; Length 53;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 3 KLVP 6

RESULT 24

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C;Species: Ovis sp. (sheep)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: E60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: E60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56130

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 21 KLVP 24

RESULT 25

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C;Accession: F60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: F60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56127; NID:gl895; PIDN:CAA9592.1; PID:gl896

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 21 KLVP 24

RESULT 26

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: G60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56126

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 21 KLVP 24

RESULT 27

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: D60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: D60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56124

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 21 KLVF 24

## RESULT 28

A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C/Species: Canis lupus familiaris (dog)  
C/Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C/Accession: A60045  
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A/Reference number: A60045; PMID:92017079; PMID:1656157  
A/Accession: A60045  
A/Molecule type: mRNA  
A/Residues: 1-57 <JOH>  
A/Cross-references: EMBL:X56125  
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 21 KLVF 24

## RESULT 29

B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C/Species: Ursus maritimus (polar bear)  
C/Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C/Accession: B60045  
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A/Reference number: A60045; PMID:92017079; PMID:1656157  
A/Accession: B60045  
A/Molecule type: mRNA  
A/Residues: 1-57 <JOH>  
A/Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166  
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 21 KLVF 24

## RESULT 30

D97742  
hypothetical protein RC0340 [imported] - Rickettsia conorii (strain Malish 7)  
C/Species: Rickettsia conorii  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
C/Accession: D97742  
R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rickettsia conorii  
Science 293, 2093-2098, 2001  
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A/Reference number: A97700; PMID:21442074; PMID:11557893  
A/Accession: D97742  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-57 <KUR>  
A/Cross-references: GB:AE006914; PIDN:AL02878.1; PID:G15619402; GSPDB:GN00173  
C/Genetics:

A/Gene: RC0340

Query Match 100.0%; Score 4; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 52 KLVF 55

## RESULT 31

B97758  
hypothetical protein RC0466 [imported] - Rickettsia conorii (strain Malish 7)  
C/Species: Rickettsia conorii  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
C/Accession: B97758  
R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rickettsia conorii  
Science 293, 2093-2098, 2001  
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A/Reference number: A97700; PMID:21442074; PMID:11557893  
A/Accession: B97758  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-67 <KUR>  
A/Cross-references: GB:AE006914; PIDN:AL03004.1; PID:G15619539; GSPDB:GN00173  
A/Genetics:

Query Match 100.0%; Score 4; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 5 KLVF 8

## RESULT 32

B33979  
peptidyl-dipeptidase A (EC 3.4.15.1) precursor (clone T11B) - human (fragment)  
N/Alternate names: peptidyl-dipeptidase I  
C/Species: Homo sapiens (man)  
C/Date: 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change 30-Jun-1995  
C/Accession: B33979  
R/Enlbers, M.R.W.; Fox, E.A.; Strydom, D.J.; Riordan, J.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989  
A/Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis  
A/Reference number: A33979; PMID:90046671; PMID:2554286  
A/Accession: B33979  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-69 <EHL>  
A/Cross-references: GB:M26658  
C/Superfamily: mammalian peptidyl-dipeptidase A  
C/Keywords: alternative splicing; peptidyl-dipeptide hydrolase; zinc

Query Match 100.0%; Score 4; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
|||  
Db 22 KLVF 25

## RESULT 33

T46201  
protein translocation complex sec61 gamma chain-like protein - Arabidopsis thaliana  
N/Alternate names: protein TBP19.80  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 02-Sep-2000  
C/Accession: T46201

R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa  
submitted to the Protein Sequence Database, December 1999  
A;Reference number: Z23008  
A;Accession: T46201  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-69 <CHO>  
A;Cross-references: EMBL:AL13315  
A;Experimental source: cultivar Columbia; BAC clone T8P19  
C;Genetics:  
A;Map position: 3  
A;Introns: 32/1  
A;Note: T8P19.80  
C;Superfamily: yeast S8S1 protein

Query Match 100.0%; Score 4; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 55 KLVP 58

RESULT 34  
AB2884  
hypothetical protein Atu2501 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
C;Accession: AB2884  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; PMID:11743193  
A;Accession: AB2884  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-71 <KUP>  
A;Cross-references: GB:AE008688; PIDN:AAL43488.1; PID:gl7740994; GSPDB:GN00186  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: Atu2501  
A;Map position: circular chromosome

Query Match 100.0%; Score 4; DB 2; Length 71;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 45 KLVP 48

RESULT 35  
S28793  
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)  
N;Alternate names: major surface antigen p190  
C;Species: Plasmodium falciparum  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000  
C;Accession: S28793  
R;Hall, R.; Hyde, J.E.; Goman, M.; Simmons, D.L.; Hope, I.A.; Mackay, M.; Scaife, J.; Me  
Nature 311, 379-382, 1984  
A;Title: Major surface antigen gene of a human malaria parasite cloned and expressed in  
A;Reference number: S28793; MUID:85012680; PMID:6090934  
A;Accession: S28793  
A;Molecule type: mRNA  
A;Residues: 1-72 <HAL>  
A;Cross-references: EMBL:M32152; NID:gl60423; PIDN:AA29658.1; PID:gl60424  
C;Superfamily: major merozoite surface antigen

C;Keywords: merozoite; surface antigen

Query Match 100.0%; Score 4; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 38 KLVP 41

# RESULT 36

A38883  
rab protein Rab6 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 02-Feb-2001  
C;Accession: A38883; JH0653  
R;Chavrier, P.; Simons, K.; Zerial, M.  
Submitted to GenBank, June 1992  
A;Reference number: A38879  
A;Accession: A38883  
A;Molecule type: mRNA  
A;Residues: 1-73 <CHA>  
A;Cross-references: GB:M79313  
R;Chavrier, P.; Simons, K.; Zerial, M.  
Gene 112, 261-264, 1992  
A;Title: The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by a  
A;Reference number: JH0639; MUID:92210010; PMID:1555775  
A;Accession: JH0653  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-2, 'T', '4-61, 'V', '63-73 <CH2>  
A;Experimental source: kidney  
C;Superfamily: ras transforming protein; translation elongation factor Tu homology  
C;Keywords: GTP binding; nucleotide binding; P-loop  
F;20-27/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 4; DB 2; Length 73;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 15 KLVP 18

# RESULT 37

S35774  
T-cell receptor alpha chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 23-Jul-1999  
C;Accession: S35774  
R;Wedderburn, L.R.  
Submitted to the EMBL Data Library, June 1993  
A;Reference number: S35769  
A;Accession: S35774  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-75 <WED>  
A;Cross-references: EMBL:Z23043; NID:g312209; PIDN:CAA80578.1; PID:g940541  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 100.0%; Score 4; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4  
|||  
Db 55 KLVP 58

# RESULT 38

B84305  
 hypothetical protein Vng1513h [imported] - Halobacterium sp. NRC-1  
 C/Species: Halobacterium sp. NRC-1  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C/Accession: B84305  
 R/Ng, W.V.; Kennedy, S.P.; Mahairs, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leitauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabic Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
 A/Title: Genome sequence of Halobacterium species NRC-1  
 A/Reference number: A84160; MUID:20504483; PMID:11016950  
 A/Accession: B84305  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-78 <STO>  
 A/Cross-references: GB:AE004437; NID:G10581004; PIDN:AA019806.1; GSPDB:GN00138  
 C/Genetics:  
 A/Gene: VNG1513H

Query Match 100.0%; Score 4; DB 2; Length 78;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 40 KLVF 43

## RESULT 39

C97829  
 hypothetical protein RC1035 [imported] - Rickettsia conorii (strain Malish 7)  
 C/Species: Rickettsia conorii  
 C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
 C/Accession: C97829  
 R/Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barde, V.; Samson, D.; R  
 Science 293, 2093-2098, 2001  
 A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
 A/Reference number: A97700; MUID:21442074; PMID:11557893  
 A/Accession: C97829  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-79 <KOR>  
 A/Cross-references: GB:AE006914; PIDN:AL03573.1; PID:G15620153; GSPDB:GN00173  
 C/Genetics:  
 A/Gene: RC1035

Query Match 100.0%; Score 4; DB 2; Length 79;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 39 KLVF 42

## RESULT 40

H71614  
 Protein translocation complex, sec61 gamma chain PFB0450w - malaria parasite (Plasmodium  
 C/Species: Plasmodium falciparum  
 C/Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 24-Sep-1999  
 C/Accession: H71614  
 R/Gardner, M.J.; Tettein, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
 Science 282, 1126-1132, 1998  
 A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
 A/Reference number: A71600; MUID:99021743; PMID:9804551  
 A/Accession: H71614  
 A/Status: preliminary;  
 A/Molecule type: DNA  
 A/Residues: 1-81 <GAR>  
 A/Cross-references: GB:AE001395; GB:AE001362; NID:G3845184; PIDN:AA071879.1; PID:G384518  
 A/Experimental source: clone 3D7

C/Genetics:  
 A/Gene: PFB0450w  
 C/Superfamily: Yeast SSS1 protein

Query Match 100.0%; Score 4; DB 2; Length 81;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 67 KLVF 70

Search completed: January 3, 2003, 07:53:27  
 Job time : 47 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:45:26 ; Search time 10 Seconds  
(without alignments)  
16.591 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 4  
Sequence: 1 KLVF 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	57	A4_PIG	Q29023 sus scrofa
2	4	100.0	57	A4_URSMA	Q29149 ursus marit
3	4	100.0	58	A4_CANPA	Q28280 canis fami
4	4	100.0	58	A4_RABIT	Q28748 oryctolagus
5	4	100.0	58	A4_SHEEP	Q28757 ovis aries
6	4	100.0	59	A4_BOVIN	Q28053 bos taurus
7	4	100.0	86	RLZ3_METUA	P54016 methanococ
8	4	100.0	91	Y909_METUA	Q58319 methanococ
9	4	100.0	94	SPC1_YEAST	P46965 saccharomyc
10	4	100.0	95	PSC3_RAT	P02780 rattus norv
11	4	100.0	109	VNS2_CVBM	P15774 bovine coro
12	4	100.0	109	VNS2_CVHOC	Q04653 human coron
13	4	100.0	110	YCX1_CHLPI	P05370 chlorella p
14	4	100.0	118	FOLB_HAEIN	P46362 haemophilus
15	4	100.0	121	R22B_YEAST	P56628 saccharomyc
16	4	100.0	122	FOLB_ECOLI	P31055 escherichia
17	4	100.0	127	CY2_RHOVI	P00083 rhodospseud
18	4	100.0	139	PABZ_STRPY	P58175 streptococc
19	4	100.0	140	PABZ_STRPN	Q9FBD0 streptococc
20	4	100.0	144	FAZ2_LACLA	Q9CHT4 lactococcusc
21	4	100.0	146	RLI3_MYCGE	P47657 mycoplasma
22	4	100.0	152	M165_ARATH	Q9C717 arabidopsis
23	4	100.0	153	MUSE_FUSNN	O8R111 fusobacteri
24	4	100.0	156	SPRT_HAEIN	P44119 haemophilus
25	4	100.0	152	FLGA_AGRIS	Q44339 agrobacteri
26	4	100.0	164	RLI0_HELPJ	Q9ZKX2 helicobacte
27	4	100.0	164	RLI0_HELPJ	P56036 helicobacte
28	4	100.0	166	BAIE_EUSBP	P19412 eubacterium
29	4	100.0	166	YBGA_CANBO	P14292 candida boi
30	4	100.0	169	YBGA_ECOLI	P24252 escherichia
31	4	100.0	176	V6B_CVPE3	P33467 feline ente
32	4	100.0	180	TAGL_BOVIN	Q9T687 bos taurus
33	4	100.0	181	ITRB_SOYBN	P01071 glycine max

34	4	100.0	186	ATPD_CVAPA	P48082 cyanophora
35	4	100.0	190	YBAY_ECOLI	P77717 escherichia
36	4	100.0	191	TERE_ALCSP	P18782 alcaligenes
37	4	100.0	191	TERE_SERMA	O52358 serratia ma
38	4	100.0	191	V611_METUA	O58028 methanococ
39	4	100.0	193	DYR_EPT4	P04382 bacterioph
40	4	100.0	193	SAR1_CAEEL	O23445 caenorhabdi
41	4	100.0	194	YDI6_HAEIN	P44159 haemophilus
42	4	100.0	198	SARA_HUMAN	O9N331 homo sapien
43	4	100.0	198	SARA_MOUSE	P36536 mus musculu
44	4	100.0	198	SARB_HUMAN	O9Y6B6 homo sapien
45	4	100.0	198	SCP2_BACSU	P81100 bacillus su
46	4	100.0	199	FLGH_THEMA	Q9XIM6 thermocoga
47	4	100.0	201	RYH1_SCHPO	P17608 schizosacch
48	4	100.0	203	KTII_SOYBN	P25372 glycine max
49	4	100.0	204	KT12_SOYBN	P25373 glycine max
50	4	100.0	205	RAB6_CAEEL	P34313 caenorhabdi
51	4	100.0	208	ATPE_MYCGE	P47643 mycoplasma
52	4	100.0	208	RB6A_HUMAN	P20340 homo sapien
53	4	100.0	208	RB6A_MOUSE	P35279 mus musculu
54	4	100.0	208	Y644_METUA	O58060 methanococ
55	4	100.0	215	ERD2_PETHY	Q9ZFN2 petunia hyd
56	4	100.0	216	ITRA_SOYBN	P01070 glycine max
57	4	100.0	219	UNG_HAEIN	P43731 haemophilus
58	4	100.0	220	EXB3_NEIGO	O06433 neisseria g
59	4	100.0	220	EXB3_NEIMA	P57027 neisseria m
60	4	100.0	220	EXB3_NEIMA	P55375 neisseria m
61	4	100.0	220	MIRA_RICDU	P13087 richadella
62	4	100.0	222	UNG_PASMU	P57807 pasteurella
63	4	100.0	224	VL73_VACCV	P07609 vaccinia vi
64	4	100.0	224	Y35A_MYCGE	Q9Z572 mycoplasma
65	4	100.0	225	VL73_POMPV	Q91566 fowipox vir
66	4	100.0	225	Y762_HAEIN	P45050 haemophilus
67	4	100.0	229	YFOL_BACSU	P40773 bacillus su
68	4	100.0	233	MSPI_PLAFD	P13827 plasmodium
69	4	100.0	236	RR2_ARATH	P56797 arabidopsis
70	4	100.0	236	RR2_MAIZE	P16037 zea mays (m
71	4	100.0	236	RR2_ORYSA	P12145 oryza sativ
72	4	100.0	236	RR2_PEA	P08241 pisum sativ
73	4	100.0	236	RR2_SPTOL	P08242 spinacia ol
74	4	100.0	236	RR2_TOBAC	P06355 nicotiana t
75	4	100.0	237	RR2_WHEAT	P17933 triticum ae
76	4	100.0	237	RR2_EPTVI	P27068 epifagus vi
77	4	100.0	243	RL7A_YEAST	P05373 saccharomyc
78	4	100.0	243	RL7B_YEAST	Q12213 saccharomyc
79	4	100.0	244	BOS1_YEAST	P25385 saccharomyc
80	4	100.0	251	RL7C_SCHPO	O60143 schizosacch
81	4	100.0	252	PHNK_ECOLI	P16578 escherichia
82	4	100.0	252	YRY2_CAEEL	Q10006 caenorhabdi
83	4	100.0	253	YR24_MYCTU	P71593 mycobacteri
84	4	100.0	253	YTRQ_BACSU	P53560 bacillus su
85	4	100.0	258	GRAM_RAT	Q03338 rattus norv
86	4	100.0	258	MIP_CHLPI	Q9Z7P3 chlamydia p
87	4	100.0	268	KSGA_RICPR	P00552 r dimethyla
88	4	100.0	270	YG12_BACUT	P10023 bacillus th
89	4	100.0	280	FDHC_METTP	O50568 methanobact
90	4	100.0	280	FDHC_METTP	P35839 methanobact
91	4	100.0	280	Y356_MYCGE	Q49437 mycoplasma
92	4	100.0	281	MSPI_PLAFN	P13320 plasmodium
93	4	100.0	282	Y356_MYCPN	P73420 mycoplasma
94	4	100.0	283	Y595_MYCTU	Q10816 mycobacteri
95	4	100.0	287	RL6_HUMAN	O08278 homo sapien
96	4	100.0	287	RL6_MOUSE	P47811 mus musculu
97	4	100.0	293	RL6_MOUSE	Q49937 spinacia ol
98	4	100.0	293	RL6_MOUSE	Q9ZM31 helicobacte
99	4	100.0	296	Y347_HELPJ	P21333 rattus norv
100	4	100.0	297	TOXD_COCOA	O54006 cochllobol
101	4	100.0	298	PANE_BACSU	Q34651 bacillus su
102	4	100.0	298	Y812_ARCFU	O29946 archaeoglob
103	4	100.0	300	SHM1_YEAST	P38988 saccharomyc
104	4	100.0	303	RICCN	Q92186 ticketstia
105	4	100.0	305	E2BA_CAEEL	P34604 caenorhabdi
106	4	100.0			

107	4	100.0	306	1	PPT1_MOUSE	O88531	mus musculus	180	4	100.0	415	1	IDHC_TOBAC	P50218	nicotiana t
108	4	100.0	306	1	PPT1_RAT	P45479	rattus norv	181	4	100.0	416	1	IDHC_SOLTU	P50217	solanum tub
109	4	100.0	312	1	BSPA_POPDE	Q07469	populus del	182	4	100.0	417	1	AGP_PRORE	Q52309	providencia
110	4	100.0	312	1	BSPB_POPE	Q09117	populus del	183	4	100.0	417	1	PGK2_RHINI	P29406	rhizopus ni
111	4	100.0	314	1	VP23_HSVB	P28921	equine herp	184	4	100.0	417	1	PGK_YARLI	P29407	yarrowia li
112	4	100.0	315	1	UNG_PRVIF	P52506	pseudorabie	185	4	100.0	417	1	RPOB_SAPOF	P08036	saponaria o
113	4	100.0	316	1	UNG_PRVKA	P52507	pseudorabie	186	4	100.0	421	1	CLPX_CHLPN	Q92760	chlamydia p
114	4	100.0	321	1	CYF_GUTH	Q78494	guillardia	187	4	100.0	421	1	FP3_BOVIN	P48830	bos taurus
115	4	100.0	323	1	FLIM_PSEAE	Q51465	pseudomonas	188	4	100.0	421	1	FP3_PIG	P42098	sus scrofa
116	4	100.0	323	1	HIS1_ARCFU	O29665	archaeoglob	189	4	100.0	422	1	FP3_MESAU	P23491	mesocricetu
117	4	100.0	325	1	MTEL_ECOLI	P00472	escherichia	190	4	100.0	423	1	PUR6_CAEEL	Q10457	c probabile
118	4	100.0	331	1	OTOC_CLOPE	O46169	clostridium	191	4	100.0	426	1	HISX_AQUAE	O66976	aquifex aeo
119	4	100.0	334	1	Y293_BUCAL	P57380	buchnera ap	192	4	100.0	426	1	FP3_CANFA	P48831	canis famli
120	4	100.0	335	1	FIMH_SALTY	P37925	salmonella	193	4	100.0	430	1	DGOT_ECOLI	P31457	escherichia
121	4	100.0	335	1	WMAT_MEASA	P35976	measles vir	194	4	100.0	432	1	ILSH_METJA	Q60296	methanococ
122	4	100.0	335	1	WMAT_MEASA	P06942	measles vir	195	4	100.0	433	1	IDHP_MEDSA	Q40345	medicago sa
123	4	100.0	335	1	WMAT_MEASH	P18611	measles vir	196	4	100.0	435	1	HEM1_LISMO	Q92bf7	listeria in
124	4	100.0	335	1	WMAT_MEASH	P26034	measles vir	197	4	100.0	435	1	HEM1_LISMO	Q8V6X4	listeria mo
125	4	100.0	335	1	WMAT_MEASU	P13844	measles vir	198	4	100.0	437	1	Y118_BORBU	O51145	borrelia bu
126	4	100.0	335	1	WMAT_RINDR	P41358	rinderpest	199	4	100.0	438	1	EFIA_DESMO	P41503	desulfuroco
127	4	100.0	342	1	H182_ARCFU	O28255	archaeoglob	200	4	100.0	442	1	ILRI_ARATH	P54968	arabidopsis
128	4	100.0	343	1	WMAT_SSPVB	P16628	subacute sc	201	4	100.0	442	1	SR54_METTH	O27376	methanobact
129	4	100.0	343	1	YOKA_BACSU	P54564	bacillus su	202	4	100.0	442	1	TRME_MYCPU	Q98rj5	mycoplasma
130	4	100.0	344	1	CDK7_CARAU	P51953	carassius a	203	4	100.0	445	1	ALCP_BACP3	P30145	bacillus ps
131	4	100.0	346	1	HIS8_VIBCH	Q9K8X2	vibrio chol	204	4	100.0	447	1	SR54_SULSO	P30145	sulfobus
132	4	100.0	346	1	Y043_BORBU	O51072	borrelia bu	205	4	100.0	448	1	YJ94_YEAST	P47159	saccharomyc
133	4	100.0	347	1	PF12_PLAFA	P19259	plasmodium	206	4	100.0	451	1	PHT1_PSEPU	Q05181	pseudomonas
134	4	100.0	349	1	RNFD_PASMU	Q9CNP3	pasteurella	207	4	100.0	451	1	SR54_ACIAM	P70722	acidianus a
135	4	100.0	350	1	GAE2_CVATE	O65781	cyamopsis t	208	4	100.0	453	1	ST24_YEAST	P47154	saccharomyc
136	4	100.0	351	1	H182_THETN	O8r5G4	thermoanaer	209	4	100.0	456	1	MANB_SALTY	P26341	salmonella
137	4	100.0	351	1	YXN1_YEAST	P53860	saccharomyc	210	4	100.0	457	1	VIPR_MELGA	Q91085	meleagris g
138	4	100.0	352	1	PSBD_CHILVU	P56319	chlorella v	211	4	100.0	461	1	ENGA_MYCLE	Q49884	mycobacteri
139	4	100.0	352	1	PSBD_NEPOL	Q9T100	nephroselm	212	4	100.0	461	1	YA01_HUMAN	Q95521	homo sapien
140	4	100.0	353	1	GBQ_DROME	P23625	drosophila	213	4	100.0	468	1	CAC2_YEAST	Q04199	saccharomyc
141	4	100.0	353	1	GBQ_HOMAM	P91950	homarus ame	214	4	100.0	468	1	MA3R_YEAST	P38157	saccharomyc
142	4	100.0	353	1	HIS7_BUCAL	P57203	buchnera ap	215	4	100.0	469	1	DLDH_CHLVI	O50311	chlorobium
143	4	100.0	357	1	PIRD_MYCTU	O06236	mycobacteri	216	4	100.0	470	1	ACHP_CHICK	P26153	gallus gall
144	4	100.0	358	1	PHO2_YARLI	P30887	yarrowia li	217	4	100.0	471	1	Y123_MYCGE	P47369	mycoplasma
145	4	100.0	358	1	TRMU_SYNY3	P73755	synecocyst	218	4	100.0	472	1	C901_ARATH	Q42569	arabidopsis
146	4	100.0	359	1	GB11_XENLA	P43444	xenopus lae	219	4	100.0	474	1	YA05_HUMAN	O60811	homo sapien
147	4	100.0	360	1	TRMU_HELPJ	Q92JG0	helicobacte	220	4	100.0	476	1	LIPB_PSEFL	P41773	pseudomonas
148	4	100.0	360	1	TRMU_HELPY	O25893	helicobacte	221	4	100.0	477	1	GATB_MYCGE	P47346	mycoplasma
149	4	100.0	360	1	UXUA_THEMEA	Q9WX84	thermotoga	222	4	100.0	477	1	RT3D_ACTPL	Q08633	actinobacil
150	4	100.0	360	1	UXUA_THEME	Q60040	thermotoga	223	4	100.0	478	1	GSA_TOBAC	P31593	nicotiana t
151	4	100.0	362	1	HIS8_XANCP	P58892	xanthomonas	224	4	100.0	479	1	APRA_PSEAE	Q03023	pseudomonas
152	4	100.0	363	1	HIS8_XANAC	P58891	xanthomonas	225	4	100.0	479	1	ICB8_HUMAN	Q14790	h caspase-8
153	4	100.0	365	1	HIS8_XYLPA	Q9PBC6	xyella fas	226	4	100.0	479	1	NUN2_RHIME	P56911	rhizobium m
154	4	100.0	366	1	DPRG_GERHY	P51105	gerbera hyb	227	4	100.0	486	1	ZYVL_CAEEL	Q21276	caenorhabdi
155	4	100.0	368	1	GBAE_CAEEL	Q5B192	caenorhabdi	228	4	100.0	487	1	TRKH_HAEIN	P44843	haemophilus
156	4	100.0	370	1	GBA2_KULUA	P54111	kluyveromyc	229	4	100.0	491	1	FBP_BACSU	P39844	bacillus su
157	4	100.0	372	1	NUIC_SYNY3	P26522	synecocyst	230	4	100.0	495	1	GLC1_SOYBN	P04776	glycine max
158	4	100.0	373	1	GLNA_CRILQ	P04773	cricetulus	231	4	100.0	496	1	CEB3_CAEVU	P45436	caenorhabdi
159	4	100.0	373	1	GLNA_PIG	P46410	sus scrofa	232	4	100.0	500	1	YJGR_ECOLI	P39342	escherichia
160	4	100.0	373	1	GLNA_FAT	P09606	rattus norv	233	4	100.0	503	1	AMPA_VIBCH	Q9K2W5	vibrio chol
161	4	100.0	374	1	YHNG_YEAST	P38797	saccharomyc	234	4	100.0	506	1	VP7_RDVFP	Q85435	rice dwarf
162	4	100.0	378	1	ALGL_PSEBS	Q17P2	pseudomonas	235	4	100.0	507	1	CP77_MOUSE	P27786	mus musculus
163	4	100.0	380	1	APG2_ARCFU	O28847	archaeoglob	236	4	100.0	507	1	CP77_RAT	P11715	rattus norv
164	4	100.0	380	1	Y420_METJA	Q57863	methanococ	237	4	100.0	518	1	YL92_YEAST	P18634	saccharomyc
165	4	100.0	381	1	NANH_SALTY	P29768	salmonella	238	4	100.0	519	1	LEUI_XYLPA	Q9PC93	xyella fas
166	4	100.0	384	1	SCS7_YEAST	Q03529	saccharomyc	239	4	100.0	520	1	LEUI_XANCP	P58900	xanthomonas
167	4	100.0	387	1	YGZ6_YEAST	P33063	saccharomyc	240	4	100.0	520	1	LEUI_XANCP	P58901	xanthomonas
168	4	100.0	392	1	NADD_UREPA	Q9PQ21	ureaplasma	241	4	100.0	522	1	C9C1_DROME	Q9W130	drosophila
169	4	100.0	395	1	METL_HUMAN	Q00266	homo sapien	242	4	100.0	523	1	IDHP_MOUSE	P54071	mus musculus
170	4	100.0	397	1	METL_RAT	P13444	rattus norv	243	4	100.0	539	1	PPB_LYSEN	Q05205	lysobacter
171	4	100.0	401	1	GPCI_METJA	Q59000	methanococ	244	4	100.0	548	1	ADEC_BORBU	O50821	borrelia bu
172	4	100.0	401	1	PNCB_YERPE	Q8Z993	versinia pe	245	4	100.0	554	1	SYQ_SALTI	Q828f8	salmonella
173	4	100.0	404	1	RPAL_SALTY	P26471	salmonella	246	4	100.0	554	1	SYQ_SALTY	Q828X5	salmonella
174	4	100.0	404	1	THII_STRPY	Q9A088	streptococ	247	4	100.0	554	1	YGS6_YEAST	P46945	saccharomyc
175	4	100.0	408	1	RATC_CAEEL	Q22067	caenorhabdi	248	4	100.0	558	1	LEUI_CIOAB	Q97mc5	clostridium
176	4	100.0	409	1	YNE4_CAEEL	P30643	caenorhabdi	249	4	100.0	565	1	ESR3_MICUN	P06773	microgogoni
177	4	100.0	411	1	RRI_SPIOI	P29344	spinacia ol	250	4	100.0	565	1	RAD7_YEAST	P06779	saccharomyc
178	4	100.0	413	1	HEM1_COXBU	P47846	coxiella bu	251	4	100.0	567	1	CYDC_BACSU	P94366	bacillus su
179	4	100.0	413	1	IDHC_SOYBN	Q06197	glycine max	252	4	100.0	568	1	ERB1_CARAU	Q9W669	carassius a

180	4	100.0	415	1	IDHC_TOBAC	P50218	nicotiana t
181	4	100.0	416	1	IDHC_SOLTU	P50217	solanum tub
182	4	100.0	417	1	AGP_PRORE	Q52309	providencia
183	4	100.0	417	1	PGK2_RHINI	P29406	rhizopus ni
184	4	100.0	417	1	PGK_YARLI	P29407	yarrowia li
185	4	100.0	417	1	RPOB_SAPOF	P08036	saponaria o
186	4	100.0	421	1	CLPX_CHLPN	Q92760	chlamydia p
187	4	100.0	421	1	FP3_BOVIN	P48830	bos taurus
188	4	100.0	421	1	FP3_PIG	P42098	sus scrofa
189	4	100.0	422	1	FP3_MESAU	P23491	mesocricetu
190	4	100.0	423	1	PUR6_CABEL	Q10457	c probabile
191	4	100.0	426	1	HISX_AQUAE	O66976	aquifex aeo
192	4	100.0	426	1	FP3_CANFA	P48831	canis famli
193	4	100.0	430	1	DGOT_ECOLI	P31457	escherichia
194	4	100.0	432	1	TISH_METJA	Q60296	methanococc
195	4	100.0	433	1	IDHP_MEDSA	Q40345	medicago sa
196	4	100.0	435	1	HEM1_LISIN	Q92bf7	listeria in
197	4	100.0	435	1	HEM1_LISMO	Q8y6x4	listeria mo
198	4	100.0	437	1	YL18_BORBU	OS1145	borrelia bu
199	4	100.0	438	1	EF1A_DESMO	P41203	desulfuroco
200	4	100.0	442	1	ILR1_ARATH	P54968	arabidopsis
201	4	100.0	442	1	SR54_METTH	O27376	methanobact
202	4	100.0	442	1	TRME_MYCPU	Q98rj5	mycoplasma
203	4	100.0	445	1	ALCP_EACP3	P30145	bacillus ps
204	4	100.0	447	1	SR54_SULSO	Q97ze7	sulfolobus
205	4	100.0	448	1	YJ94_YEAST	Q07159	saccharomyc
206	4	100.0	451	1	PHY1_PSEPU	Q05181	pseudomonas
207	4	100.0	451	1	SR54_ACIAM	P70722	acidianus a
208	4	100.0	453	1	SW24_YEAST	P47154	saccharomyc
209	4	100.0	456	1	MANB_SALTY	P26341	salmonella
210	4	100.0	457	1	Y1PR_MELGA	Q91085	meleagris g
211	4	100.0	461	1	ENGA_MYCLE	Q43884	mycobacteri
212	4	100.0	461	1	YA01_HUMAN	O95521	homo sapien
213	4	100.0	468	1	CAC2_YEAST	Q0a199	saccharomyc
214	4	100.0	468	1	MA3R_YEAST	P38157	saccharomyc
215	4	100.0	469	1	LDH8_CHLVI	O50311	chlorobium
216	4	100.0	470	1	ACHP_CHICK	P26153	gallus gall
217	4	100.0	471	1	Y123_MYCCE	P47369	mycoplasma
218	4	100.0	472	1	C901_ARATH	Q42569	arabidopsis
219	4	100.0	474	1	YA05_HUMAN	O60811	homo sapien
220	4	100.0	476	1	LIPB_PSEFL	P41773	pseudomonas
221	4	100.0	477	1	GATB_MYCGE	P47346	mycoplasma
222	4	100.0	477	1	RT3D_ACTPL	Q08633	actinobacil
223	4	100.0	478	1	GSA_TOBAC	P31593	nicotiana t
224	4	100.0	479	1	APR8_PSEAE	Q03023	pseudomonas
225	4	100.0	479	1	ICB8_HUMAN	O14790	h caspase-8
226	4	100.0	479	1	NUN2_RHIME	P56911	rhizobium m
227	4	100.0	486	1	TRVL_CAEEL	Q21276	caenorhabdi
228	4	100.0	487	1	ZYKH_HAEIN	P44843	haemophilus
229	4	100.0	491	1	PBP_BACSU	P39844	bacillus su
230	4	100.0	495	1	GLC1_SOYBN	P04776	glycine max
231	4	100.0	496	1	CED3_CAEVU	P45436	caenorhabdi
232	4	100.0	500	1	YUGR_ECOLI	P39342	escherichia
233	4	100.0	503	1	AMPA_VIBCH	Q9K2w5	vibrio chol
234	4	100.0	506	1	VP7_RDVF	Q85435	rice dwarf
235	4	100.0	507	1	CPT7_MOUSE	P27786	mus musculus
236	4	100.0	507	1	CPT7_RAT	P11715	rattus norv
237	4	100.0	518	1	YL92_YEAST	P18634	saccharomyc
238	4	100.0	519	1	LEU1_XYLFA	Q9pcg3	xyliella fas
239	4	100.0	520	1	LEU1_XANAC	P58900	xanthomonas
240	4	100.0	520	1	LEU1_XANCP	P58901	xanthomonas
241	4	100.0	522	1	C9C1_DROME	Q9w130	drosophila
242	4	100.0	523	1	IDHP_MOUSE	P54071	mus musculus
243	4	100.0	539	1	PPB_LYSEN	Q05205	lysobacter
244	4	100.0	548	1	ADSC_BORBU	O50821	borrelia bu
245	4	100.0	554	1	SYQ_SALT1	O8x8f8	salmonella
246	4	100.0	554	1	SYQ_SALT2	P482qx5	salmonella
247	4	100.0	554	1	YGS6_YEAST	P45945	saccharomyc
248	4	100.0	558	1	LEU1_CLOAB	Q97mc5	clostridium
249	4	100.0	565	1	ESP3_MICUN	P57783	micropongi
250	4	100.0	565	1	RAD7_YEAST	P06779	saccharomyc
251	4	100.0	567	1	CYDC_BACSU	P43466	bacillus su
252	4	100.0	568	1	ERB1_CARAU	Q9w669	caerulus a



253	4	100.0	568	1	MET3_ASPT6	P56862	aspergillus	326	4	100.0	788	1	PAB3_YEAST	P37254	saccharomyc
254	4	100.0	572	1	MET3_PENCH	Q12650	penicillium	327	4	100.0	794	1	SYO_LUPLU	P52780	lupinus lut
255	4	100.0	572	1	SYK_CAEEL	Q22099	caenorhabd	328	4	100.0	797	1	PKP3_MOUSE	P57126	mus musculus
256	4	100.0	573	1	ILTV_HAEIN	P45261	haemophilus	329	4	100.0	803	1	GYRB_BUCAL	P75793	buchnera ap
257	4	100.0	574	1	MET3_EMENT	O12555	emericella	330	4	100.0	810	1	PRPF_ECOLI	P75793	escherichia
258	4	100.0	576	1	MUTL_CHLTR	O84579	chlamydia t	331	4	100.0	810	1	UP05_ECOLI	P39170	escherichia
259	4	100.0	584	1	COAT_PAVC2	P30109	canine parv	332	4	100.0	820	1	SYL_CHLPP	Q92330	chlamydia p
260	4	100.0	586	1	RPOC_EUGRG	P23580	euglena gra	333	4	100.0	830	1	YG02_YEAST	P40627	saccharomyc
261	4	100.0	586	1	RT67_ECOLI	P21325	escherichia	334	4	100.0	833	1	CASL_MOUSE	Q35177	mus musculus
262	4	100.0	588	1	YA71_SCHPO	Q09758	schizosacch	335	4	100.0	834	1	CASL_HUMAN	O14511	homo sapien
263	4	100.0	589	1	PEX8_YEAST	P53248	saccharomyc	336	4	100.0	836	1	MCBL_SEVKA	P25550	shope fibro
264	4	100.0	591	1	Y040_MYCGE	P47286	mycoplasma	337	4	100.0	859	1	TLRS_MOUSE	Q911E7	mus musculus
265	4	100.0	594	1	IF2P_MERTH	O26339	methanobact	338	4	100.0	870	1	ADH2_ENTHI	Q24603	entamoeba h
266	4	100.0	596	1	NUOL_CAMJE	O9pmat7	campylobact	339	4	100.0	874	1	BCA1_HUMAN	P55465	homo sapien
267	4	100.0	613	1	ISP6_CHLPP	O92810	chlamydia p	340	4	100.0	874	1	BCA1_MOUSE	O61140	mus musculus
268	4	100.0	618	1	SL55_RAT	O63008	rattus norv	341	4	100.0	881	1	DPOL_HPRGS	P03161	ground squi
269	4	100.0	621	1	FOR_THRELI	O56303	thermococcu	342	4	100.0	882	1	HELI_HSV11	P10189	herpes simp
270	4	100.0	622	1	AMAI_PLAF8	P50492	plasmodium	343	4	100.0	882	1	HSS1_HUMAN	P52548	homo sapien
271	4	100.0	622	1	AMAI_PLAF6	P50489	plasmodium	344	4	100.0	883	1	HSS1_RAT	Q02353	rattus norv
272	4	100.0	622	1	AMAI_PLAF6	P22621	plasmodium	345	4	100.0	883	1	HSS2_MOUSE	P52850	mus musculus
273	4	100.0	622	1	AMAI_PLAF6	P50490	plasmodium	346	4	100.0	886	1	CHS_SAPMO	P48017	saprolegnia
274	4	100.0	622	1	AMAI_PLAFH	P50491	plasmodium	347	4	100.0	902	1	NRC4_HUMAN	O14834	homo sapien
275	4	100.0	630	1	VI09_FOMPV	P36317	lowipox vir	348	4	100.0	904	1	PPR1_YEAST	P07272	saccharomyc
276	4	100.0	632	1	ETPD_SCHPO	P87111	s probable	349	4	100.0	906	1	RPOL_BPK11	P18147	bacterioph
277	4	100.0	633	1	NODO_RHISB	O07309	r nodg bifu	350	4	100.0	909	1	Y4G1_RHISN	P55465	rhizobium s
278	4	100.0	640	1	SCAA_RABIT	O97741	oryctolagus	351	4	100.0	926	1	POB1_YEAST	Q01454	saccharomyc
279	4	100.0	641	1	NODO_RHIME	P13442	r nodg bifu	352	4	100.0	932	1	YATA_SCHPO	O09897	schizosacch
280	4	100.0	647	1	NTPI_MSEPV	O9y429	melanoplus	353	4	100.0	939	1	YL09_YEAST	O06678	saccharomyc
281	4	100.0	647	1	TOP3_VIBCH	O9kgf5	vibrio chol	354	4	100.0	966	1	CAPP_MEDSA	Q02735	medicago sa
282	4	100.0	648	1	TALA_POWMK	P24597	mouse polyo	355	4	100.0	967	1	CAPP_SOYBN	P51061	glycine max
283	4	100.0	650	1	SCAA_BOVIN	P55270	bos taurus	356	4	100.0	967	1	CAPP_PEA	P51062	pisum sativ
284	4	100.0	650	1	Y873_MYCTU	O10535	mycobacteri	357	4	100.0	967	1	HEPA_ECOLI	P23852	escherichia
285	4	100.0	653	1	EGLN_PIG	P37176	sus scrofa	358	4	100.0	968	1	BCA1_RAT	O63767	rattus norv
286	4	100.0	658	1	REP_BUCAP	O51889	buchnera ap	359	4	100.0	969	1	AGU1_SCHPO	O9c0y4	schizosacch
287	4	100.0	664	1	Y366_MYCPN	P75234	mycoplasma	360	4	100.0	978	1	PEX6_RAT	P54777	rattus norv
288	4	100.0	667	1	Y366_MYCGE	P47606	mycoplasma	361	4	100.0	980	1	PEX6_HUMAN	Q13308	homo sapien
289	4	100.0	669	1	SCAA_HUMAN	P37088	homo sapien	362	4	100.0	1017	1	DPOL_ADEB2	O72539	bovine aden
290	4	100.0	682	1	DY12_CHLRE	Q39578	chlamydomon	363	4	100.0	1018	1	SYL_ARCFU	O29622	archaeoglob
291	4	100.0	683	1	LCPE_RAT	O88813	rattus norv	364	4	100.0	1019	1	LFC_TACTR	P28175	tachyples
292	4	100.0	684	1	XYNA_CALSR	P40944	caldicellulu	365	4	100.0	1023	1	CI0C_DROME	O61735	drosophila
293	4	100.0	687	1	GALK_KULTA	P09609	kluveromyc	366	4	100.0	1033	1	YD56_SCHPO	Q10309	schizosacch
294	4	100.0	690	1	ATM1_YEAST	P40416	saccharomyc	367	4	100.0	1038	1	BGAL_ALTRA	P81560	alteromonas
295	4	100.0	695	1	GFA1_SCHPO	Q09740	schizosacch	368	4	100.0	1053	1	RPOC_LISGR	P77882	listeria gr
296	4	100.0	696	1	CAT1_PENNA	P81138	penicillium	369	4	100.0	1059	1	CAPP_DROME	Q24120	drosophila
297	4	100.0	698	1	SCAA_RAT	P37089	rattus norv	370	4	100.0	1061	1	DPOL_ADE12	P06533	human adeno
298	4	100.0	699	1	SCAA_MOUSE	O61180	mus musculus	371	4	100.0	1065	1	RPOB_MARPO	P06272	marthantia
299	4	100.0	700	1	YDHV_ECOLI	P76192	escherichia	372	4	100.0	1070	1	RPOB_SPTOL	P11703	spinacia ol
300	4	100.0	702	1	CANB_HUMAN	Q9umg6	homo sapien	373	4	100.0	1070	1	RPOB_TOBAC	P06271	nicotiana t
301	4	100.0	705	1	C1R_HUMAN	P00736	homo sapien	374	4	100.0	1072	1	RPOB_ARATH	P50546	arabidopsis
302	4	100.0	705	1	BEFG_XYLPA	Q9p390	xyloella fas	375	4	100.0	1072	1	RPOB_OENHO	O9umt5	oenothera h
303	4	100.0	707	1	NRDD_HAEIN	P43752	haemophilus	376	4	100.0	1075	1	NFC3_HUMAN	O12368	homo sapien
304	4	100.0	711	1	TRPL_HUMAN	P02788	homo sapien	377	4	100.0	1075	1	NFC3_MOUSE	P97305	mus musculus
305	4	100.0	712	1	NRDD_ECOLI	Q91646	salmonella	378	4	100.0	1075	1	RPOB_WAIZE	P16023	zea mays (m
306	4	100.0	712	1	NRDD_SALTY	O35350	mus musculus	379	4	100.0	1075	1	RPOB_ORYZA	P12091	oryza sativ
307	4	100.0	713	1	CAN1_MOUSE	P97571	rattus norv	380	4	100.0	1076	1	RPOB_PINTH	O9x067	pinus thunb
308	4	100.0	713	1	CAN1_RAT	P07384	homo sapien	381	4	100.0	1076	1	RPOB_WHEAT	O9x067	triticum ae
309	4	100.0	714	1	CAN1_HUMAN	P35750	homo sapien	382	4	100.0	1082	1	RPOB_SIGNAL	P46618	sinapis alb
310	4	100.0	714	1	CAN1_PIG	P27437	mus scrofa	383	4	100.0	1101	1	RPOB_ROTIC	P26190	porcine rot
311	4	100.0	722	1	COAT_MEVA	P04863	canine parv	384	4	100.0	1101	1	KOBS_YEAST	Q08217	saccharomyc
312	4	100.0	722	1	COAT_PAVC7	P32323	saccharomyc	385	4	100.0	1120	1	MPD_RICPR	O05555	riceletisia
313	4	100.0	725	1	AGAI_YEAST	P04864	canine parv	386	4	100.0	1122	1	DPOL_ADE07	P05664	human adeno
314	4	100.0	727	1	COAT_FPV	P24840	canine parv	387	4	100.0	1140	1	DDB1_CERAE	P33194	herpes simp
315	4	100.0	727	1	COAT_FPV19	Q11213	canine parv	388	4	100.0	1140	1	DDB1_HUMAN	O16531	c data damag
316	4	100.0	727	1	COAT_PAVCB	P17455	canine parv	389	4	100.0	1150	1	DPOL_ADECT	P87553	canine aden
317	4	100.0	748	1	COAT_PAVCN	P12930	canine parv	390	4	100.0	1151	1	XPO4_HUMAN	Q9ce10	homo sapien
318	4	100.0	751	1	A4_SATSC	Q95241	saimiri sci	391	4	100.0	1176	1	HYMDH_PHYBL	Q12849	phycomyc
319	4	100.0	770	1	A4_HUMAN	P05067	homo sapien	392	4	100.0	1181	1	Y002_METUA	O60301	methanococ
320	4	100.0	770	1	A4_MOUSE	P12023	mus musculus	393	4	100.0	1193	1	DPOL_ADE04	P87503	human adeno
321	4	100.0	770	1	A4_RAT	P08592	rattus norv	394	4	100.0	1193	1	YPERB_BACSU	P54159	bacillus su
322	4	100.0	773	1	Z341_HUMAN	Q9Bdy7	homo sapien	395	4	100.0	1199	1	RPOC_BACSU	P37871	bacillus su
323	4	100.0	775	1	SYO_HUMAN	P47897	homo sapien	396	4	100.0	1227	1	LAF4_HUMAN	P51826	homo sapien
324	4	100.0	780	1	PPSA_DEIRA	O83026	deinococcus	397	4	100.0	1237	1	POL4_DROME	P10394	drosophila
325	4	100.0						398	4	100.0					

399	4	100.0	1288	1	CTA3_HUMAN	Q9bz76	homo sapien	472	3	75.0	36	1	PSAI_MAIZE	P30380	zea mays (m
400	4	100.0	1331	1	Y064_MYCGE	P47310	mycoplasma	473	3	75.0	36	1	PSAI_MESVI	Q9muq4	mesostigma
401	4	100.0	1332	1	XDH_HUMAN	P47989	homo sapien	474	3	75.0	36	1	PSAI_NEPOL	Q9t112	nephroselm
402	4	100.0	1374	1	VCAP_HSV11	P06491	herpes simp	475	3	75.0	36	1	PSAI_ORYSA	P12186	oryza sativ
403	4	100.0	1380	1	SP14_YEAST	P36126	saccharomyc	476	3	75.0	36	1	PSAI_TOBAC	P21187	nicotiana t
404	4	100.0	1386	1	Y064_MYCPN	P75613	mycoplasma	477	3	75.0	36	1	PSAI_WHEAT	P25410	tritium ae
405	4	100.0	1396	1	VCAP_VZVD	P09245	varicella-z	478	3	75.0	37	1	PSAI_ARATH	P56768	arabidopsis
406	4	100.0	1587	1	SUR2_CABEL	Q10689	caenorhabdi	479	3	75.0	38	1	HOXH_RHOOP	P22861	rhodococcus
407	4	100.0	1616	1	YAED_SCHPO	Q09853	schizosacch	480	3	75.0	40	1	PHRX_BACSU	O31840	bacillus su
408	4	100.0	1630	1	MSPI1_PLAFK	P04932	plasmodium	481	3	75.0	40	1	PMP1_YEAST	P32903	saccharomyc
409	4	100.0	1639	1	MSPI1_PLAFW	P04933	plasmodium	482	3	75.0	42	1	GBG7_MOUSE	Q61016	mus musculus
410	4	100.0	1682	1	MSPI1_PLAF3	P19598	plasmodium	483	3	75.0	42	1	RS7_STAAR	P48940	staphylococ
411	4	100.0	1691	1	POLN_HEVME	Q03495	hepatitis e	484	3	75.0	43	1	PM2_YEAST	P40975	saccharomyc
412	4	100.0	1693	1	POLN_HEVBU	P29324	hepatitis e	485	3	75.0	43	1	VES_PAPVE	P11330	european el
413	4	100.0	1693	1	POLN_HEVPA	Q04610	hepatitis e	486	3	75.0	44	1	GGI3_STAHA	P11699	staphylococ
414	4	100.0	1693	1	POLN_HEVPA	P33424	hepatitis e	487	3	75.0	44	1	RL34_CAUCR	P58129	caulobacter
415	4	100.0	1713	1	LMA3_HUMAN	Q16787	homo sapien	488	3	75.0	44	1	RL34_RHILO	Q98490	rhizobium l
416	4	100.0	1726	1	MSPI1_PLAPC	P04934	plasmodium	489	3	75.0	44	1	RL34_RHIME	Q928f3	rhizobium m
417	4	100.0	1726	1	MSPI1_PLAPP	P50495	plasmodium	490	3	75.0	44	1	VE5_PAPVR	P21403	reindeer pa
418	4	100.0	1741	1	RPC1_GIALA	P25202	giardia lam	491	3	75.0	45	1	RL36_CHLPN	Q928x0	chlamydia p
419	4	100.0	1807	1	VT42_XENLA	P18709	xenopus lae	492	3	75.0	45	1	RL36_CHLTR	O84791	chlamydia t
420	4	100.0	1852	1	RPB1_CABEL	P16356	caenorhabdi	493	3	75.0	46	1	SR7A_STRPY	Q9f4v1	streptococc
421	4	100.0	1885	1	PAS2_CANAL	P43098	c fatty aci	494	3	75.0	48	1	YCX9_CVAPA	P48330	cyanophora
422	4	100.0	2026	1	CYAA_YEAST	P08678	saccharomyc	495	3	75.0	48	1	YK82_ARCFU	P48197	archaeoglob
423	4	100.0	2127	1	RRPL_RABVS	P16289	rabies viru	496	3	75.0	49	1	COX4_PARDE	P77921	paracoccus
424	4	100.0	2142	1	RRPL_RABVP	P11213	rabies viru	497	3	75.0	49	1	YBHT_ECOLI	P75759	escherichia
425	4	100.0	2199	1	DPOE_SCHPO	P87154	schizosacch	498	3	75.0	50	1	REPA_BPT4	P32284	bacterioph
426	4	100.0	2871	1	DESP_HUMAN	P15924	homo sapien	499	3	75.0	50	1	RL39_KLUMA	P48536	kluyveromyc
427	4	100.0	3080	1	POLG_ZYMVC	P18479	z genome po	500	3	75.0	51	1	DHE3_ELEEL	P28270	electrophor
428	4	100.0	3083	1	POLG_ZYMVS	Q36979	z genome po	501	3	75.0	51	1	R27A_METTH	O26368	methanobact
429	4	100.0	3092	1	IRAI_YEAST	P18963	saccharomyc	502	3	75.0	51	1	VG62_BMD2	O64354	mycobacteri
430	4	100.0	4466	1	DYHC_ANTCR	P39057	anthocidari	503	3	75.0	52	1	NU3M_NEUCR	Q35141	neurospora
431	4	100.0	4540	1	DYHC_PARTE	Q77171	paramecium	504	3	75.0	53	1	Y870_ARCFU	O29931	archaeoglob
432	3	75.0	7	1	CCF1_ENTFPA	P20104	enterococcu	505	3	75.0	53	1	YK11_TRYBB	P02300	trypanosoma
433	3	75.0	10	1	RCA_PINPS	P81084	pinus pinas	506	3	75.0	54	1	ATP8_CARAU	O78683	carassius a
434	3	75.0	13	1	CRBL_VESLE	P17235	vespula lew	507	3	75.0	54	1	ATP8_CYPCA	P24948	cyprinus ca
435	3	75.0	13	1	CRTC_RANES	P1832	rana escul	508	3	75.0	54	1	ATP8_ECOLI	P02436	escherichia
436	3	75.0	14	1	CRBL_VESOR	P17236	rana escul	509	3	75.0	55	1	ATP8_GROLA	P34190	crossostoma
437	3	75.0	17	1	BOL4_MEGPE	P07495	megabombus	510	3	75.0	55	1	ATP8_ONCMY	P48179	oncorhynch
438	3	75.0	19	1	TPIS_CLOPRA	P81348	clostridium	511	3	75.0	55	1	ATP8_PAROL	Q9t9d5	paralichthy
439	3	75.0	19	1	UP27_UPEMJ	P82039	uperoleia m	512	3	75.0	55	1	ATP8_SALAL	Q9xn27	salvelinus
440	3	75.0	20	1	VI01_VACCV	P16714	vaccinia vi	513	3	75.0	55	1	ATP8_SALFO	Q9xn35	salvelinus
441	3	75.0	23	1	PS3_ESEPD	P83190	pseudis par	514	3	75.0	55	1	ATP8_SQUAC	Q92250	squalus aca
442	3	75.0	23	1	PS4_PSEPD	P83191	pseudis par	515	3	75.0	55	1	LHB_RHOTE	P80387	rhodocyci
443	3	75.0	23	1	UDP_LACCA	P19662	lactobacill	516	3	75.0	55	1	P628_HUMAN	Q9u154	homo sapien
444	3	75.0	24	1	RAN_XENLA	P52301	xenopus lae	517	3	75.0	55	1	RL33_YERPE	Q8z1p1	yersinia pe
445	3	75.0	26	1	PCW4_PACGO	P82426	pachycondyl	518	3	75.0	56	1	RL33_PASMU	P57912	pasteurella
446	3	75.0	27	1	LPRM_STREN	P21233	streptococc	519	3	75.0	56	1	Y048_BORBU	O51077	borrelia bu
447	3	75.0	27	1	LSP_APIME	P09355	apis mellif	520	3	75.0	57	1	SCPI_MESMA	Q9u8d2	mesobuthus
448	3	75.0	29	1	KDPF_ECOLI	P36937	escherichia	521	3	75.0	57	1	SECE_HALNI	Q9hs72	halobacteri
449	3	75.0	30	1	AATC_RABIT	P12343	oryctolagus	522	3	75.0	57	1	V3A_IBVM	P05137	avian infec
450	3	75.0	30	1	DMS3_PHYSA	P80279	phyllomedus	523	3	75.0	57	1	V3A_IBVU3	P30238	avian infec
451	3	75.0	31	1	PMGY_CANAL	P82612	candida alb	524	3	75.0	57	1	V3A_IBVU4	P30239	avian infec
452	3	75.0	31	1	H13_WHEAT	P15872	tritium ae	525	3	75.0	57	1	V3A_IBVU5	P30240	avian infec
453	3	75.0	31	1	LPRM_ECOLI	P10739	escherichia	526	3	75.0	57	1	YAC2_LSGPN	P37034	legionella
454	3	75.0	32	1	COA2_BP1F1	O80296	bacterioph	527	3	75.0	58	1	LHAI_RHOCA	P02948	rhodobacter
455	3	75.0	32	1	CRP_EPLEF	P12245	pleuronecte	528	3	75.0	58	1	V3A_IBVB	P02937	avian infec
456	3	75.0	32	1	FF21_SALEN	P55224	salmonella	529	3	75.0	58	1	VPU_HV12H	P08806	human immu
457	3	75.0	32	1	PETL_CHLRE	P50369	chlamydomon	530	3	75.0	58	1	Y121_NPVAC	P41674	autographa
458	3	75.0	33	1	PSAI_SPIOL	P17228	spinacia ol	531	3	75.0	58	1	YV48_PVRAB	Q9V126	pyrococcus
459	3	75.0	34	1	COXA_THETH	P82543	thermus the	532	3	75.0	59	1	Y288_RICPR	Q9Zdn9	rickettsia
460	3	75.0	34	1	PSAI_LOTJA	Q9db80	lotus japon	533	3	75.0	59	1	YHDO_ECOLI	P45764	escherichia
461	3	75.0	34	1	PSAI_OENHO	Q9nt12	oenothera h	534	3	75.0	60	1	CX1_NAJME	P01455	naja haja a
462	3	75.0	34	1	PSAI_SOYEN	P49159	glycine max	535	3	75.0	60	1	CX1_NAJNI	P01448	naja melano
463	3	75.0	35	1	SPICL_SPIPL	P72506	spiralina p	536	3	75.0	60	1	CX1_NAJOX	P01456	naja nivea
464	3	75.0	35	1	SCCK_TITSE	P56219	titivus serr	537	3	75.0	60	1	CX1_NAJOX	P01451	naja oxiana
465	3	75.0	35	1	TXH4_SELHU	P83303	selenocosmi	538	3	75.0	60	1	CX2_NAJHA	P01462	naja haja a
466	3	75.0	35	1	YC12_CYACA	Q9c1x0	cyanidium c	539	3	75.0	60	1	CX2_NAJHA	P01440	naja haja a
467	3	75.0	36	1	LPRM_ENTFPA	P23130	enterococcu	540	3	75.0	60	1	CX3_NAJOX	P01441	naja oxiana
468	3	75.0	36	1	PSAI_ANGLY	P28251	angiopteris	541	3	75.0	60	1	CX3_NAJHA	P01459	naja haja a
469	3	75.0	36	1	PSAI_BRAOL	Q31909	brassica ol	542	3	75.0	60	1	CX5T_NAJAT	P07525	naja atra
470	3	75.0	36	1	PSAI_CHLVU	P58214	chlorella v	543	3	75.0	60	1	CX5_NAJHA	P01464	naja haja a
471	3	75.0	36	1	PSAI_HORVU	P13165	hordeum vul	544	3	75.0	60	1	CX6_NAJHA	P01465	naja haja a

545	3	75.0	60	1	CX7_NAJIA	P01466 najia haje a	618	3	75.0	68	1	Y055_NPVOP	O10133 oryza pseu
546	3	75.0	60	1	CX8_NAJIA	P01460 najia haje a	619	3	75.0	69	1	GBG7_RAT	P43425 rattus norv
547	3	75.0	60	1	CX9_NAJIA	P01454 najia haje a	620	3	75.0	69	1	LHB_RHORI	P04125 rhodospiril
548	3	75.0	60	1	RL30_THETH	P74909 thermus the	621	3	75.0	69	1	NS2C_HUMAN	O14961 homo sapien
549	3	75.0	60	1	SECE_STAAM	O06442 staphylococ	622	3	75.0	69	1	YVDE_VACCV	P04341 vaccinia vi
550	3	75.0	60	1	Y072_NPVAC	P41471 autographa	622	3	75.0	70	1	GBG2_MOUSE	P16874 mus musculu
551	3	75.0	61	1	CX1_HEMIA	P01471 hemachatus	624	3	75.0	70	1	MEL_APIME	P01501 apia mellif
552	3	75.0	61	1	CX3_HEMIA	P24777 methachatus	625	3	75.0	70	1	RL29_METUA	P54303 methanococc
553	3	75.0	61	1	SASA_BACME	P02959 bacillus me	626	3	75.0	70	1	SAS1_CIOBI	P22065 clostridium
554	3	75.0	61	1	Y737_METUA	O58147 methanococc	627	3	75.0	70	1	UBIL_CAEBR	O07371 caenorhabdi
555	3	75.0	61	1	YCFC9_ODOI	P49528 odontella s	628	3	75.0	70	1	V43_BPT3	P20317 bacterioph
556	3	75.0	62	1	CECA_TRINI	P50724 trichoplus	629	3	75.0	70	1	Y3C4_STRCO	O53866 streptomyce
557	3	75.0	62	1	IOIA_GONVI	P82025 gonatodes v	630	3	75.0	70	1	Y216_METUA	O60263 methanococ
558	3	75.0	62	1	RL19_METH	O26894 methanobact	631	3	75.0	71	1	ARRD_RAT	P36577 rattus norv
559	3	75.0	62	1	RL19_MAIZE	O80866 zea mays (m	632	3	75.0	71	1	ATPL_ENTHR	P26682 enterococcu
560	3	75.0	62	1	STAT_HUMAN	P02808 homo sapien	633	3	75.0	71	1	CHH1_MACRS	P81206 macrobrachi
561	3	75.0	62	1	YCFC9_ARATH	P56780 arabidopsis	634	3	75.0	71	1	ESSD_ECOLI	P77242 escherichia
562	3	75.0	62	1	YCFC9_CHLRE	P92276 chlamydomon	635	3	75.0	71	1	ESSQ_ECOLI	P77237 escherichia
563	3	75.0	62	1	YCFC9_CHLVU	P56313 chlorella v	636	3	75.0	71	1	PABM_CHICK	P80565 gallus gall
564	3	75.0	62	1	YCFC9_LOTJA	O9bbr2 lotus japon	637	3	75.0	71	1	HP12_ECTVA	P38524 ectothiorho
565	3	75.0	62	1	YCFC9_MAIZE	O33300 zea mays (m	638	3	75.0	71	1	RL31_THEMA	O54311 thermotoga
566	3	75.0	62	1	YCFC9_MARPO	P09973 marchantia	639	3	75.0	71	1	SASC_BACME	P02860 bacillus me
567	3	75.0	62	1	YCFC9_MESVI	O8ump9 mesostigma	640	3	75.0	71	1	TATR_XYLPA	O9plu3 xylella fas
568	3	75.0	62	1	YCFC9_MEPOL	O9tKx2 neptoseimi	641	3	75.0	71	1	VGE_SPV4	P11338 spiroplasma
569	3	75.0	62	1	YCFC9_OENHO	O9mtt5 oenothera h	642	3	75.0	71	1	YC47_PORPU	P51574 porphyra pu
570	3	75.0	63	1	YCFC9_ORYSA	P12194 oryza sativ	643	3	75.0	71	1	YB35_METUA	O58830 methanococ
571	3	75.0	62	1	YCFC9_PEA	O32902 pisum sativ	644	3	75.0	71	1	YRL5_MYCCA	P43040 mycoplasma
572	3	75.0	62	1	YCFC9_SPIOLO	O9m3m6 spinacia ol	645	3	75.0	72	1	CHH6_PENUP	P81700 penaeus jap
573	3	75.0	62	1	YCFC9_TOBAC	P09974 nicotiana t	646	3	75.0	72	1	HP11_ECTVA	P38841 ectothiorho
574	3	75.0	62	1	YCFC9_WHEAT	P08890 triticum ae	647	3	75.0	72	1	HTF_BLDI	Q17128 biaberus di
575	3	75.0	63	1	ATP8_BALMU	P41292 balaeoptera	648	3	75.0	72	1	PEN2_PENVA	P24833 human papil
576	3	75.0	63	1	CE3D_HYPCU	P50720 hyphantria	649	3	75.0	72	1	VES_HPV3	P81057 penaeus van
577	3	75.0	63	1	PSBH_SYNY3	P14835 synchocyst	650	3	75.0	72	1	VP13_BPPH6	P11330 bacterioph
578	3	75.0	64	1	ANP1_PHRDE	P35751 rhigophila	651	3	75.0	72	1	Y111_NPVOP	O10351 oryza pseu
579	3	75.0	64	1	BD01_PIG	O62637 sus scrofa	652	3	75.0	72	1	Y541_BORBU	O51491 borrelia bu
580	3	75.0	64	1	SAS2_CIOBI	P22066 clostridium	653	3	75.0	72	1	YF77_HAEIN	Q57070 haemophilus
581	3	75.0	64	1	SAS4_BACSU	P04833 bacillus su	654	3	75.0	73	1	CHH_JASIA	P56687 jaesus jalan
582	3	75.0	64	1	Y05X_BPT4	P39238 bacterioph	655	3	75.0	73	1	MALE_PHOLO	P41130 photorhabdu
583	3	75.0	64	1	YC33_SKECO	O96808 ekeletonema	656	3	75.0	73	1	PSPD_ECOLI	P23856 escherichia
584	3	75.0	65	1	YC33_GURTH	O78517 guillardia	657	3	75.0	73	1	UL12_HCMVA	P16777 human cytom
585	3	75.0	65	1	YCFC9_EUGER	P32035 euglena gra	658	3	75.0	73	1	VES_HPV18	P06792 human papil
586	3	75.0	66	1	ATPL_STOR	P50017 streptococc	659	3	75.0	73	1	VSH_BRSA	P24616 bovine resp
587	3	75.0	66	1	ATPL_STREP	O59953 streptococc	660	3	75.0	73	1	Y055_NPVAC	P41555 autographa
588	3	75.0	66	1	CLUS_SHEEP	P17698 ovie aries	661	3	75.0	73	1	YPO4_NPVLD	P30326 lymphotria d
589	3	75.0	66	1	DMS5_PACDA	O93455 pachymedusa	662	3	75.0	74	1	ABL_CALVI	P11681 calliphora
590	3	75.0	66	1	PLI2_VYREN	P52429 yerenia en	663	3	75.0	74	1	DEF2_CAPAN	O65740 capsicum an
591	3	75.0	66	1	V07K_WCMVM	P09501 white clove	664	3	75.0	74	1	RPOZ_HELPY	O025467 helicobacte
592	3	75.0	66	1	V07K_WCMVO	P15405 white clove	665	3	75.0	74	1	SRP_SOYBN	O07502 glycine max
593	3	75.0	66	1	YVAR_VACCC	P20527 vaccinia vi	666	3	75.0	74	1	Y131_MYCGE	O29721 archaeoglob
594	3	75.0	66	1	YICD_BACSU	P37480 bacillus su	667	3	75.0	74	1	Y529_ARCFU	P37533 bacillus su
595	3	75.0	67	1	CERC_CERCA	O17313 ceratitidis c	668	3	75.0	74	1	YVAL_BACSU	P37533 bacillus su
596	3	75.0	67	1	PSBH_ODOI	P49475 odontella s	669	3	75.0	75	1	DEPL_CAPAN	Q43413 capsicum an
597	3	75.0	67	1	YCFC9_ANASP	P80558 anabena sp	670	3	75.0	75	1	YCEK_ECOLI	P454052 escherichia
598	3	75.0	67	1	YCFC9_MASLA	P20116 masligoclad	671	3	75.0	76	1	RLX_METUA	P54052 methanococ
599	3	75.0	67	1	PYC1_SYNEP6	P50036 synchococc	672	3	75.0	76	1	SIFA_ARATH	P42551 arabidopsis
600	3	75.0	67	1	PYC1_SYNEP	P06114 synchococc	673	3	75.0	76	1	SECG_MYCPN	O9e450 mycoplasma
601	3	75.0	67	1	PYC1_SYNY4	O01950 synchocyst	674	3	75.0	76	1	V419_VARY	P33842 varicola vit
602	3	75.0	67	1	PYC1_SYNY4	O02925 synchocyst	675	3	75.0	77	1	PIIF_BOMPO	Q10731 bombyx mori
603	3	75.0	67	1	RL17E_PIRAB	O9v050 pyrococcus	676	3	75.0	77	1	MULI_SERMA	P02338 serratia ma
604	3	75.0	67	1	RL17E_PIRFU	O8u0u1 pyrococcus	677	3	75.0	77	1	NXP4_MACMU	O8umj7 macaca mula
605	3	75.0	67	1	RL17E_PIRFO	P58503 pyrococcus	678	3	75.0	77	1	TACI_TACTR	P14213 tachepleus
606	3	75.0	67	1	RL29_THETH	O91cy4 thermus the	679	3	75.0	77	1	TAC2_TACTR	P14213 tachepleus
607	3	75.0	67	1	RL30_THEMA	O9x111 thermotoga	680	3	75.0	77	1	V419_VACCC	P20994 vaccinia vi
608	3	75.0	67	1	RL31_TREPA	O66075 treponema p	681	3	75.0	77	1	VNSB_CXH22	P19741 human coron
609	3	75.0	67	1	RPOZ_LISIN	O92a12 listeria in	682	3	75.0	77	1	Y084_TREPA	O83122 treponema p
610	3	75.0	67	1	RPOZ_LISMO	O8y673 listeria mo	683	3	75.0	77	1	Y184_METUA	O57432 methanococ
611	3	75.0	67	1	Y158_RICPR	O28604 rickettsia	684	3	75.0	77	1	Y4DJ_RHISN	P55409 rhibobium s
612	3	75.0	67	1	YF82_ARCFU	O28690 archaeoglob	685	3	75.0	77	1	Y812_RICPR	O92e04 rickettsia
613	3	75.0	68	1	YPUB_BACSU	P35151 bacillus su	686	3	75.0	77	1	YC34_CVAPA	P48374 cyanophora
614	3	75.0	68	1	GBG7_BOVIN	P30671 bos taurus	687	3	75.0	77	1	YQ17_ARCFU	O28856 archaeoglob
615	3	75.0	68	1	GBG7_HUMAN	O60262 homo sapien	688	3	75.0	77	1	YQ41_BACAN	O9mz1 bacillus an
616	3	75.0	68	1	MRSA_BACSP	P43663 bacillus sp	689	3	75.0	78	1	IF1_MYCPN	O50298 mycoplasma
617	3	75.0	68	1	PYC1_FREDDI	P16569 fremyella d	690	3	75.0	78	1	MULI_ECOLI	P02937 escherichia

691	3	75.0	78	1	MULI_ERWAM	P02939	erwinia amy	764	3	75.0	85	1	SCI5_MESMA	Q9ng98 mesobuthus
692	3	75.0	78	1	RS20_STRPN	Q97zh7	scitococc	765	3	75.0	85	1	SCAL_MESMA	Q9gyx2 mesobuthus
693	3	75.0	78	1	VE5_HPV10	P50774	human papil	766	3	75.0	85	1	YNAJ_ECOLI	P76050 escherichia
694	3	75.0	78	1	VG9_SPV1R	P15900	spiroplasma	767	3	75.0	86	1	GON2_ONCMY	P04241 oncorhynch
695	3	75.0	78	1	V43_CVPPU	P04136	porcine tra	768	3	75.0	86	1	ILVM_ECOLI	P13048 escherichia
696	3	75.0	78	1	Y43_BPR51	P18244	bacterioph	769	3	75.0	86	1	IMM2_ECOLI	P04482 escherichia
697	3	75.0	78	1	YDH2_PLAFL	P14588	plasmodium	770	3	75.0	86	1	IMM9_ECOLI	P13479 escherichia
698	3	75.0	78	1	YDHI_ECOLI	P76184	escherichia	771	3	75.0	86	1	ISK4_MOUSE	P35579 mus musculus
699	3	75.0	79	1	ACP2_PSEAE	P52658	pseudomonas	772	3	75.0	86	1	RL23_METVA	P10143 methanococ
700	3	75.0	79	1	CKS1_HUMAN	P33551	homo sapien	773	3	75.0	86	1	SELW_HUMAN	O15532 homo sapien
701	3	75.0	79	1	PINH_ECOLI	P76611	escherichia	774	3	75.0	86	1	SELW_PIG	Q95kl4 sus scrofa
702	3	75.0	79	1	RL11_DICDI	P16168	dictyosteli	775	3	75.0	86	1	SELM_SHEEP	O19097 ovis aries
703	3	75.0	79	1	RS16_BUCAI	P57474	buchnera ap	776	3	75.0	86	1	SPAQ_SALTY	P40704 salmonella
704	3	75.0	79	1	SU11_CHICK	P51971	gallus gall	777	3	75.0	86	1	VE7_HPV10	P36818 human papil
705	3	75.0	79	1	YD5B_YEAST	P56508	saccharomyc	778	3	75.0	86	1	YABO_BACSU	P37557 bacillus su
706	3	75.0	79	1	YF31_HELPY	O26059	helicobacte	779	3	75.0	87	1	BC10_HUMAN	O60629 homo sapien
707	3	75.0	80	1	AFPI_ARATH	P30224	arabidopsis	780	3	75.0	87	1	FYX3_HUMAN	Q14802 homo sapien
708	3	75.0	80	1	ELBB_KLEPN	O48464	klebsiella	781	3	75.0	87	1	NULM_APILI	P34959 apis mellif
709	3	75.0	80	1	ICTA_SYNY3	P27372	synecocyst	782	3	75.0	87	1	RS18_THETH	P80382 thermus the
710	3	75.0	80	1	R31B_XYLFA	Q9pd45	xyliella fas	783	3	75.0	87	1	SELM_MOUSE	P49904 mus musculus
711	3	75.0	80	1	S61G_YEAST	P35179	saccharomyc	784	3	75.0	88	1	HIPB_ECOLI	P23873 escherichia
712	3	75.0	80	1	VPU_HV1WA	P05924	human immun	785	3	75.0	88	1	HKL2_MAIZE	P56659 zea mays (m
713	3	75.0	80	1	YKQ_BPP22	P57018	bacterioph	786	3	75.0	88	1	MINE_GUIHE	O78435 guilladia
714	3	75.0	80	1	YTO8_MYCLE	Q33015	mycobacteri	787	3	75.0	88	1	PTHG_MYCGE	P47287 mycoplasma
715	3	75.0	81	1	CK1B_NAJAT	Q98956	naja atra (	788	3	75.0	88	1	PTHG_MYCPN	P75961 mycoplasma
716	3	75.0	81	1	CK1_NAJATP	Q02454	naja sputat	789	3	75.0	88	1	RS15_BORBU	O51744 borrelia bu
717	3	75.0	81	1	CK2_NAJAT	P01442	naja atra (	790	3	75.0	88	1	SCAB_CANFA	Q95165 canis famil
718	3	75.0	81	1	CK3A_NAJAT	Q98959	naja atra (	791	3	75.0	88	1	V184_FOWPV	Q9j549 fowlpox vir
719	3	75.0	81	1	CK3B_NAJAT	Q98960	naja atra (	792	3	75.0	88	1	VK03_VACCC	P20639 vaccinia vi
720	3	75.0	81	1	CK3_NAJAT	P01444	naja atra (	793	3	75.0	88	1	VK03_VACCV	P18378 vaccinia vi
721	3	75.0	81	1	CK4_NAJAT	P01443	naja atra (	794	3	75.0	88	1	Y073_BACHD	O9k918 bacillus ha
722	3	75.0	81	1	CK5_NAJAT	Q98961	naja atra (	795	3	75.0	89	1	BXB2_BOMMO	P26774 bombyx mori
723	3	75.0	81	1	MCPI_HIRME	P81511	hirudo medi	796	3	75.0	89	1	FLIQ_AQUAE	O67774 axylefex aeo
724	3	75.0	81	1	PN3C_PENVA	P81060	penaeus van	797	3	75.0	89	1	PTHG_XYLFA	Q9dh66 xyliella fas
725	3	75.0	81	1	VK06_VACCV	P18381	vaccinia vi	798	3	75.0	89	1	PTSN_PSEPU	P33670 pseudomonas
726	3	75.0	81	1	VPU_HV1EL	P05925	human immun	799	3	75.0	89	1	R14B_LACLA	Q9ch51 lactococcus
727	3	75.0	81	1	VPU_HV1ND	P18806	human immun	800	3	75.0	89	1	RS15_CHLPN	O92698 chlamydia p
728	3	75.0	81	1	VSH_BR5V3	P25515	human immun	801	3	75.0	89	1	RS15_CHLTR	O84850 chlamydia t
729	3	75.0	81	1	YCZI_BAGSU	P32554	bovine resp	802	3	75.0	89	1	RS20_MYCPU	Q98pr3 mycoplasma
730	3	75.0	81	1	C5Z1_BAGSU	P42970	bacillus su	803	3	75.0	89	1	TATA_HAEIN	P57046 haemophilus
731	3	75.0	82	1	C551_AZOV1	P00104	azotobacter	804	3	75.0	89	1	VAPI_RTEAN	O85172 riemerella
732	3	75.0	82	1	C551_PSEDE	P00103	pseudomonas	805	3	75.0	89	1	YC02_PARDE	P08302 paracoccus
733	3	75.0	82	1	C551_PSEME	P00102	pseudomonas	806	3	75.0	89	1	YR88_MYCCA	P43047 mycoplasma
734	3	75.0	82	1	P212_MERUN	Q99pe3	meriones un	807	3	75.0	89	1	CC2_PETHY	P43290 petunia hyb
735	3	75.0	82	1	P8_HUMAN	O60356	homo sapien	808	3	75.0	90	1	EF1B_AERPE	Q9y304 aeropyrum p
736	3	75.0	82	1	PN3A_PENVA	P81058	penaeus van	809	3	75.0	90	1	IM09_EMENI	Q9y8a7 emericeila
737	3	75.0	82	1	PN3B_PENVA	P81059	penaeus van	810	3	75.0	90	1	PTHG_PSEPU	Q92426 pseudomonas
738	3	75.0	82	1	TXAL_ACTEQ	Q9njq2	actinia equ	811	3	75.0	90	1	RS15_CAMJE	P49392 campylobact
739	3	75.0	82	1	Y9K2_SSVI	P20200	sulfolobus	812	3	75.0	90	1	RS15_HELPY	Q92m39 helicobacte
740	3	75.0	82	1	YBDJ_ECOLI	P77506	escherichia	813	3	75.0	90	1	RS15_BOMMO	P56022 helicobacte
741	3	75.0	82	1	YBDJ_KLEPN	O48414	klebsiella	814	3	75.0	91	1	DEFV_MOUSE	P15410 bombyx mori
742	3	75.0	82	1	YD4_IBVK	P19745	avian infec	815	3	75.0	91	1	DEFV_MOUSE	P50716 mus musculu
743	3	75.0	82	1	YDCX_ECOLI	P76109	escherichia	816	3	75.0	91	1	DEFV_MOUSE	P50715 mus musculu
744	3	75.0	83	1	OADG_KLEPN	P13155	klebsiella	817	3	75.0	91	1	DEFV_MOUSE	O64263 mus musculu
745	3	75.0	83	1	OADG_PASMU	Q9cl26	pasteurella	818	3	75.0	91	1	DEFV_MOUSE	P17534 mus musculu
746	3	75.0	83	1	TRBG_ECOLI	P41072	escherichia	819	3	75.0	91	1	EF1B_SULTO	Q976h8 sulfolobus
747	3	75.0	83	1	YCIN_ECOLI	P46132	escherichia	820	3	75.0	91	1	GATC_BORBU	O51318 borrelia bu
748	3	75.0	83	1	YF24_ARCFU	O28748	archaeoglob	821	3	75.0	91	1	NDC2_BRAJA	P53418 bradyrhizob
749	3	75.0	83	1	Y102_CVEM	P22054	bovine coro	822	3	75.0	91	1	UTER_HUMAN	P03475 influenza a
750	3	75.0	84	1	NXP4_HUMAN	Q95158	homo sapien	823	3	75.0	91	1	VC15_VACCC	P11694 homo sapien
751	3	75.0	84	1	RPOH_SULAC	P11521	sulfolobus	824	3	75.0	91	1	Y257_ARCFU	P21099 vaccinia vi
752	3	75.0	84	1	UL73_HSV6U	Q976a3	sulfolobus	825	3	75.0	91	1	Y257_ARCFU	O29982 archaeoglob
753	3	75.0	84	1	UL73_HSV6Z	Q60694	human herpe	826	3	75.0	92	1	CXAI_PIG	Q29101 sus scrofa
754	3	75.0	84	1	Y076_NPVAC	P52547	human herpe	827	3	75.0	92	1	DY1_RHOTE	P00098 rhodocyclu
755	3	75.0	84	1	Y076_NPVOP	Q06690	autographa	828	3	75.0	92	1	CYL1_YEAST	O02647 saccharomyc
756	3	75.0	84	1	Y8_SOCMV	O10329	orgyia pseeu	829	3	75.0	92	1	NODF_RHLIV	P04665 rhizobium l
757	3	75.0	84	1	YQ13_BACAN	Q9rn19	bacillus chl	830	3	75.0	92	1	PLM_HUMAN	O00168 homo sapien
758	3	75.0	84	1	Y576_MYCLE	Q9cbu2	mycobacteri	831	3	75.0	92	1	PTHG_STRCO	O50515 streptomyce
759	3	75.0	85	1	Y576_MYCLE	P00097	rhodocyclu	832	3	75.0	92	1	PTSO_VIBCH	Q9rk46 vibrio chol
760	3	75.0	85	1	HKL7_MAIZE	P56664	zea mays (m	833	3	75.0	92	1	RS18_DEIRA	Q9y350 deinococcus
761	3	75.0	85	1	HKL7_MAIZE	P56665	zea mays (m	834	3	75.0	92	1	SP12_ARATH	Q94410 arabidopsis
762	3	75.0	85	1	RS17_MYCGA	O52341	mycoplasma	835	3	75.0	92	1	AAT_METEX	P52069 methylobact
763	3	75.0	85	1				836	3	75.0	93	1		

837	3	75.0	93	1	DEF1_MOUSE	P11477	mus musculus	910	3	75.0	98	1	NUM_BALMU	P41301	balaeoptex
838	3	75.0	93	1	DEF5_RAT	P82106	rattus norv	911	3	75.0	98	1	NUM_BALPH	P24976	balaeoptex
839	3	75.0	93	1	FXF8_HUMAN	P58550	homo sapien	912	3	75.0	98	1	NUM_BOVIN	P03902	bos taurus
840	3	75.0	93	1	IM10_YEAST	P87108	saccharomyc	913	3	75.0	98	1	NUM_CANFA	Q92259	canis famli
841	3	75.0	93	1	IM12A_MEDSA	Q04361	medicago sa	914	3	75.0	98	1	NUM_CERSI	Q03203	ceratotheri
842	3	75.0	93	1	UGR1_HUMAN	Q26p11	homo sapien	915	3	75.0	98	1	NUM_DIDMA	P41307	didelphis m
843	3	75.0	93	1	VE7_HPVI5	P36820	human papil	916	3	75.0	98	1	NUM_EQUAS	P92483	equus asinu
844	3	75.0	93	1	VE7_HPVI4	P27231	human papil	917	3	75.0	98	1	NUM_FELCA	P48931	felis silve
845	3	75.0	93	1	YNDH_RHOCA	P42030	rhodobacter	918	3	75.0	98	1	NUM_GORGO	Q34572	gorilla gor
846	3	75.0	93	1	YPM8_YEAST	Q14464	saccharomyc	919	3	75.0	98	1	NUM_HIHAM	Q92273	hipopotamu
847	3	75.0	93	1	FXF6_MOUSE	Q9d164	mus musculus	920	3	75.0	98	1	NUM_HORSE	P48658	equus caball
848	3	75.0	94	1	FXF6_RAT	Q91xw6	rattus norv	921	3	75.0	98	1	NUM_HUMAN	P03901	homo sapien
849	3	75.0	94	1	NAG7_HUMAN	Q9y6c7	homo sapien	922	3	75.0	98	1	NUM_HYLLA	Q34579	hylobates l
850	3	75.0	94	1	NRAM_IATKR	P03476	influenza a	923	3	75.0	98	1	NUM_LUMTE	Q34948	lumbricus t
851	3	75.0	94	1	V093_FOPRV	Q915c7	fowlpox vir	924	3	75.0	98	1	NUM_MACRO	P92667	macropus ro
852	3	75.0	94	1	VAP2_RIBAN	Q85171	riemereella	925	3	75.0	98	1	NUM_MICPE	Q21520	microtus pe
853	3	75.0	94	1	Y753_TREPA	Q83734	creponema p	926	3	75.0	98	1	NUM_PANPA	Q36457	ornithorhyn
854	3	75.0	94	1	YC76_ARCFU	P248992	archaeoglob	927	3	75.0	98	1	NUM_PANPA	Q35588	pan paniscu
855	3	75.0	94	1	YE93_HABIN	P44218	haemophilus	928	3	75.0	98	1	NUM_PANTR	Q37809	pan troglod
856	3	75.0	94	1	ATPJ_YEAST	P81449	saccharomyc	929	3	75.0	98	1	NUM_PAPHA	Q92xw6	papio hamad
857	3	75.0	95	1	BXC2_BOWMO	P26735	bombyx mori	930	3	75.0	98	1	NUM_PHOSU	Q21514	phodopus su
858	3	75.0	95	1	BXFI_BOWMO	P91896	bombyx mori	931	3	75.0	98	1	NUM_PROVI	Q00844	phoca vitul
859	3	75.0	95	1	FABL_CHAVI	P82145	chaetophrac	932	3	75.0	98	1	NUM_PIG	P56632	sus scrofa
860	3	75.0	95	1	FXF6_HUMAN	Q9h0g3	homo sapien	933	3	75.0	98	1	NUM_PONPY	Q35585	pongo pygma
861	3	75.0	95	1	MYLE_HUMAN	O95424	homo sapien	934	3	75.0	98	1	NUM_RABIT	Q79435	oryctolagus
862	3	75.0	95	1	NOOB_THETH	O9wug7	mus musculus	935	3	75.0	98	1	NUM_RAT	P05507	rattus norv
863	3	75.0	95	1	RELE_ECOLI	P07008	escherichia	936	3	75.0	98	1	NUM_RHUN	Q78754	ovis aries
864	3	75.0	95	1	RLZ5_HABIN	P45281	haemophilus	937	3	75.0	98	1	NUM_SHEEP	Q21567	sigmodon hi
865	3	75.0	95	1	YAJ2_SCHPO	P13324	bacterioph	938	3	75.0	98	1	NUM_SIGHI	Q91zhe	caenorhabdi
866	3	75.0	95	1	Y07B_BP74	Q09902	schizosacch	939	3	75.0	98	1	PLAS_CHLFU	P00300	chlorella f
867	3	75.0	95	1	YMS6_CABEL	Q10942	caenorhabdi	940	3	75.0	98	1	RL3E_METTH	Q27127	methanobact
868	3	75.0	95	1	YXZ2_HUMAN	Q9y3y2	homo sapien	941	3	75.0	98	1	SRG1_HUMAN	Q75711	homo sapien
869	3	75.0	96	1	ABRB_BACSU	P08874	bacillus su	942	3	75.0	98	1	Y16C_BP74	Q63751	rattus norv
870	3	75.0	96	1	EUTW_SALTU	P41791	salmonella	943	3	75.0	98	1	Y16C_BP74	P22919	bacterioph
871	3	75.0	96	1	FER_APHSA	P00250	aphanothec	944	3	75.0	98	1	Y3M3_YEAST	P39559	saccharomyc
872	3	75.0	96	1	FER_LEUGL	P00225	leucaena gl	945	3	75.0	98	1	YGIU_ECOLI	Q46665	escherichia
873	3	75.0	96	1	MPG3_DACGL	P93124	dactylis gl	946	3	75.0	99	1	BXAI_SAMCY	P33718	samta synth
874	3	75.0	96	1	PEPB_ENTHI	Q24824	entamoeba h	947	3	75.0	99	1	ETBR_MACPA	Q28468	maccia faec
875	3	75.0	96	1	RASH_MESAU	Q60529	mesocricetu	948	3	75.0	99	1	FER2_APHSA	P00251	aphanothec
876	3	75.0	96	1	RASK_RAT	P08644	rattus norv	949	3	75.0	99	1	FLGM_PROMI	P96974	proteus mir
877	3	75.0	96	1	SSGA_METAN	P52752	metarhizium	950	3	75.0	99	1	PLAS_IACSA	P00290	iactuca sat
878	3	75.0	96	1	VREN_LAMBD	P03761	bacterioph	951	3	75.0	99	1	RS24_PYRAB	P09y20	pyrococcus
879	3	75.0	96	1	YFP8_SCHPO	O14067	schizosacch	952	3	75.0	99	1	RS24_PYRAB	Q8u442	pyrococcus
880	3	75.0	96	1	YNII_MERTV	P25768	methanobact	953	3	75.0	99	1	RS24_PYRAB	P58746	pyrococcus
881	3	75.0	96	1	YXIS_BACSU	P42310	bacillus su	954	3	75.0	99	1	Y233_MYCGE	P47475	mycoplasma
882	3	75.0	96	1	DEF4_HUMAN	P12838	homo sapien	955	3	75.0	99	1	Y162_STRPY	Q09y56	streptococc
883	3	75.0	97	1	EUTW_ECOLI	P77606	escherichia	956	3	75.0	100	1	NO12_VICSA	Q41701	vicia sativ
884	3	75.0	97	1	FER1_APHFL	P00244	aphanizomen	957	3	75.0	100	1	NUM_ARATH	P26551	marichantia
885	3	75.0	97	1	FER2_CVACA	P15789	cyamidzomen	958	3	75.0	100	1	NUM_MARPO	P11888	agrobacteri
886	3	75.0	97	1	FERA_ALOMA	P81372	alocasia ma	959	3	75.0	100	1	ROLA_AGRRH	Q99962	chlamydomon
887	3	75.0	97	1	FER_COLES	P00222	colocasia e	960	3	75.0	100	1	RS14_MESVI	Q8y666	mesostigma
888	3	75.0	97	1	FER_DATST	P81454	datura stra	961	3	75.0	100	1	RS14_ANASP	O8y666	anabaena sp
889	3	75.0	97	1	FER_MEDSA	P00220	medicago sa	962	3	75.0	100	1	RS14_ANASP	P52858	synecchococ
890	3	75.0	97	1	FER_SANNI	P00226	sambucus nj	963	3	75.0	100	1	RS24_METTH	Q26367	methanobact
891	3	75.0	97	1	HV56_MOUSE	P18527	mus musculus	964	3	75.0	100	1	URS3_ACTPL	O54418	actinobacil
892	3	75.0	97	1	IL18_HORSE	Q62812	equus cabal	965	3	75.0	100	1	URS3_BACPA	P41022	bacillus pa
893	3	75.0	97	1	LITUB_CHLMU	Q9PKX8	chlamydia m	966	3	75.0	100	1	URS3_CLOPE	P04667	clostridium
894	3	75.0	97	1	MINE_SYNY3	Q58839	synecchocyt	967	3	75.0	100	1	URS3_ECOLI	Q03382	escherichia
895	3	75.0	97	1	NU1M_LOOMI	Q36423	locusta mig	968	3	75.0	100	1	URS3_HABIN	P44393	haemophilus
896	3	75.0	97	1	NU1M_MOUSE	P03903	mus musculus	969	3	75.0	100	1	URS3_KLEAE	P18316	klebsiella
897	3	75.0	97	1	PLAS_DAUCS	P20422	daucus caro	970	3	75.0	100	1	URS3_KLEPN	Q02943	mycobacteri
898	3	75.0	97	1	PLAS_PETCR	P17341	petroselinu	971	3	75.0	100	1	URS3_PROMI	P17088	proteus mir
899	3	75.0	97	1	VE7_HPVI3	P50781	human papil	972	3	75.0	100	1	URS3_PROVU	P16124	proteus vul
900	3	75.0	97	1	YA45_HABIN	Q57347	haemophilus	973	3	75.0	100	1	URS3_RHIME	P42887	rhinobium m
901	3	75.0	97	1	YC40_METUA	Q58637	methanococ	974	3	75.0	100	1	URS3_SYNY3	Q55053	streptococc
902	3	75.0	98	1	CH10_BRUJE	P25968	bruceella me	975	3	75.0	100	1	V07K_NMV	P15098	narcissus m
903	3	75.0	98	1	COXB_BOVIN	P00428	bos taurus	976	3	75.0	100	1	VIN2_BP74	P03719	bacterioph
904	3	75.0	98	1	FERR_ANASP	P00254	anabaena sp	977	3	75.0	100	1			
905	3	75.0	98	1	FERR_ANAVA	P00254	anabaena va	978	3	75.0	100	1			
906	3	75.0	98	1	FERR_ALOMA	P81373	alocasia ma	979	3	75.0	100	1			
907	3	75.0	98	1	FER_NOSMU	P00253	nostoc musc	980	3	75.0	100	1			
908	3	75.0	98	1				981	3	75.0	100	1			
909	3	75.0	98	1				982	3	75.0	100	1			

983 3 75.0 100 1 YGFE\_HABIN  
 984 3 75.0 100 1 YHBQ\_ECOLI  
 985 3 75.0 100 1 YHPQ\_YEAST  
 986 3 75.0 100 1 YLQK\_BACSU  
 987 3 75.0 101 1 CBGR\_CLOAB  
 988 3 75.0 101 1 CGEC\_BACSU  
 989 3 75.0 101 1 IL8\_CAVPO  
 990 3 75.0 101 1 IL8\_FELCA  
 991 3 75.0 101 1 IL8\_RABIT  
 992 3 75.0 101 1 RK24\_GUITH  
 993 3 75.0 101 1 RS14\_BRUME  
 994 3 75.0 101 1 RS14\_CHLMU  
 995 3 75.0 101 1 RS14\_CHLTR  
 996 3 75.0 101 1 RS14\_RALSO  
 997 3 75.0 101 1 RS14\_RHIME  
 998 3 75.0 101 1 RS14\_VIBCH  
 999 3 75.0 101 1 RS24\_METJA  
 1000 3 75.0 101 1 SMD3\_YEAST

## ALIGNMENTS

RESULT 1  
 A4\_PIG  
 ID A4\_PIG STANDARD; PRT; 57 AA.  
 AC Q29023;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
 DE protein (Beta-APP) (A-beta)] (Fragment).  
 GN APP.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP TISSUE=Brain;  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC GIO (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
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 CC  
 CC EMBL; X56127; CAA39592.1; -  
 CC HSSP; P05067; IBA4.  
 CC InterPro; IPR001868; A4\_APP.  
 CC InterPro; IPR001255; Beta-APP.  
 CC Pfam; PF03494; Beta-APP; 1.  
 CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.  
 CC NON\_TER 1 1  
 CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 34 57 POTENTIAL.  
 CC NON\_TER 57 57  
 CC SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;  
 DR HSSP; P05067; IBA4.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 DR Glycoprotein; Amyloid; Neurone; Transmembrane.  
 DR NON\_TER 1 1  
 DR CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 DR DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 DR TRANSMEM 34 57 POTENTIAL.  
 DR NON\_TER 57 57  
 DR SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;  
 Query Match 100.0%; Score 4; DB 1; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 21 KLVF 24  
 RESULT 2  
 A4\_URSMA  
 ID A4\_URSMA STANDARD; PRT; 57 AA.  
 AC Q29149;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
 DE protein (Beta-APP) (A-beta)] (Fragment).  
 GN APP.  
 OS Ursus maritimus (Polar bear) (Thalartos maritimus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
 OX NCBI\_TaxID=29073;  
 RN [1]  
 RP TISSUE=Brain;  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC GIO (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
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 CC  
 CC EMBL; X56128; CAA39593.1; -  
 CC HSSP; P05067; IBA4.  
 CC InterPro; IPR001868; A4\_APP.  
 CC InterPro; IPR001255; Beta-APP.  
 CC Pfam; PF03494; Beta-APP; 1.  
 CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.  
 CC NON\_TER 1 1  
 CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 34 57 POTENTIAL.  
 CC NON\_TER 57 57  
 CC SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;  
 Query Match 100.0%; Score 4; DB 1; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 DB 21 KLVF 24  
 RESULT 3

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A4_CANFA
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
-----
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DR EMBL; X56125; CA39590.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP.1.
DR PROSITE; PS00319; A4-EXTRA; PARTIAL.
DR PROSITE; PS00320; A4-INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT NON_TER 1 1
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;

Query Match 100.0%; Score 4; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 22 KLVF 25

RESULT 4
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

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OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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DR EMBL; X56129; CA39594.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP.1.
DR PROSITE; PS00319; A4-EXTRA; PARTIAL.
DR PROSITE; PS00320; A4-INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT NON_TER 1 1
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT TRANSMEM 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8E8BA82D CRC64;

Query Match 100.0%; Score 4; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 21 KLVF 24

RESULT 5
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

```



```
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; X56130; CAA39595.1; -.
CC CC HSPSP; P05067; 1BA4.
CC CC InterPro; IPR001868; A4 APP.
CC CC InterPro; IPR001255; Beta-APP.
CC CC Pfam; PF03494; Beta-APP; 1.
CC CC PROSITE; PS00319; A4 EXTRA; PARTIAL.
CC CC PROSITE; PS00320; A4 INTRA; PARTIAL.
CC CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC CC NON_TER 1 1
CC CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 34 57 POTENTIAL.
CC CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC CC NON_TER 58 58
CC CC SEQUENCE 58 AA; 6300 MW; F434209D88BEA82D CRC64;

Query Match 100.0%; Score 4; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 21 KLVP 24

RESULT 6
A4 BOVIN STANDARD; PRT; 59 AA.
ID A4 BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; X56124; CAA39589.1; -.
CC CC HSPSP; P05067; 1BA4.
CC CC InterPro; IPR001868; A4 APP.
CC CC InterPro; IPR001255; Beta-APP.
CC CC Pfam; PF03494; Beta-APP; 1.
CC CC PROSITE; PS00319; A4 EXTRA; PARTIAL.
CC CC PROSITE; PS00320; A4 INTRA; PARTIAL.
CC CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC CC NON_TER 1 1
CC CC CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
CC CC DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 35 58 POTENTIAL.
CC CC DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
CC CC NON_TER 59 59
CC CC SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 4; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 22 KLVP 25

RESULT 7
RL23 METJA STANDARD; PRT; 86 AA.
ID RL23 METJA
AC P54016;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L23P.
GN RPL23P OR MJ0178.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OC NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kurlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073 (1996).
CC CC -!- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S RRNA
CC CC (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
CC CC -----
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CC CC -----
CC CC EMBL; U67474; AAB98163.1; -.
CC CC TIGR; MJ0178; -.
CC CC InterPro; IPR001014; Ribosomal_L23.
```



DR Pfam; PF00276; Ribosomal\_L23; 1.  
 DR ProDom; PD00114; Ribosomal\_L23; 1.  
 DR PROSITE; PS00050; RIBOSOMAL\_L23; 1.  
 KW Ribosomal protein; RNA-binding; Complete proteome.  
 SQ SEQUENCE 86 AA, 9855 MW, DE53C1A1A361697B CRC64;

Query Match 100.0%; Score 4; DB 1; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 25 KLVF 28

RESULT 8  
 Y909 META  
 ID Y909 META STANDARD; PRT; 91 AA.

AC Q58319;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein M0909.

GN M0909.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;

RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=9637999; PubMed=688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 Overbeek R., Kirkness E.F., Weinstock K.G., Nierick J.M., Glodex A.,  
 Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 Ralston M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 "complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";

RT Science 273:1058-1073(1996).  
 RL -1- SIMILARITY: TO M.JANNASCHII MJ1103.

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CC EMBL; U67534; AAB98911.1; -.  
 DR TIGR; M0909; -.  
 DR InterPro; IPR002776; DUF79.  
 DR Pfam; PF01919; DUF79; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 91 AA, 11146 MW, 4E4260B3466CD72 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 29 KLVF 32

RESULT 9  
 SPC1 YEAST  
 ID SPC1 YEAST STANDARD; PRT; 94 AA.  
 AC P46965;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Microsomal signal peptidase subunit 1 (EC 3.4.-.-).  
 GN SPC1 OR YK010BW.

OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;

RP SEQUENCE FROM N.A.  
 RC STRAIN=AB320 / ATCC 37323;  
 RX MEDLINE=96279206; PubMed=8663399;  
 RA Fang H., Panzner S., Mullins C., Hartmann E., Green N.;  
 RT "The homologue of mammalian SPC12 is important for efficient signal  
 RT peptidase activity in Saccharomyces cerevisiae.";  
 RL J. Biol. Chem. 271:16460-16465(1996).

RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c / FY1679;  
 RA de Haan M., Smit P.H.M., Grivell L.A.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PART OF THE SIGNAL PEPTIDASE COMPLEX (SPC), EXACT  
 CC FUNCTION IS NOT KNOWN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE SPC12 FAMILY.

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DR EMBL; U26257; AAC9366.1; -.  
 DR EMBL; Z49510; CAA89533.1; -.  
 DR EMBL; Z49511; CAA89535.1; -.

DR SGD; S0003770; SPC1.

KW Hydrolyase; Protease; Microsome; Endoplasmic reticulum; Transmembrane.

FT DOMAIN 1 28 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 29 49 POTENTIAL.  
 FT DOMAIN 50 50 LUMENAL (POTENTIAL).  
 FT TRANSMEM 51 71 POTENTIAL.  
 FT DOMAIN 72 94 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 94 AA, 10819 MW, 814D7C7A949BDD CRC64;

Query Match 100.0%; Score 4; DB 1; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 11 KLVF 14

RESULT 10

P8C3 RAT  
 ID P8C3 RAT STANDARD; PRT; 95 AA.

AC P02780; Q63463;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Prostatic steroid-binding protein C3 chain precursor (Prostatein  
 DE peptide C3).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=83082848; PubMed=6294095;  
 RA Parker M.G., White R., Hurst H., Needham M., Tilly R.;

"Prostatic steroid-binding protein. Isolation and characterization of C3 genes.";  
J. Biol. Chem. 258:12-15(1983).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=8323826; PubMed=6190812;  
RA Viskochil D.H., Perry S.T., Lea O.A., Stafford D.W., Wilson E.M.,  
French F.S.;  
RA "Isolation of two genomic sequences encoding the Mr = 14,000 subunit of rat prostatein.";  
J. Biol. Chem. 258:8861-8866(1983).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=92165796; PubMed=1537831;  
RA Tan J.A., Marschke K.B., Ho K.-C., Perry S.T., Wilson E.M.,  
French F.S.;  
RA "Response elements of the androgen-regulated C3 gene.";  
J. Biol. Chem. 267:4456-4466(1992).  
[4]  
ERRATUM.  
MEDLINE=92218467; PubMed=1339454;  
RA Tan J.A., Marschke K.B., Ho K.C., Perry S.T., Wilson E.M.,  
French F.S.;  
RA J. Biol. Chem. 267:7958-7958(1992).  
[5]  
SEQUENCE OF 19-95.  
MEDLINE=81188769; PubMed=7014218;  
RA Peeters B., Rombaerts W., Mous J., Heyns W.;  
RA "Structural studies on rat prostatic binding protein. The primary structure of its glycosylated component C3.";  
Eur. J. Biochem. 115:115-121(1981).  
CC -!- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY GLYCOPROTEIN OF VENTRAL PROSTATE GLAND. STEROID-BINDING PROTEIN; CAN BIND NON-POLAR STEROIDS, CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.  
CC -!- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED C1, C2 AND C3. THESE FORM COVALENT C1:C3 (P) AND C2:C3 (S) HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC (C1:C3/C3:C2) PROSTATEIN MOLECULES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: VENTRAL PROSTATE.  
CC -!- INDUCTION: ANDROGEN DEPENDENT, AS SHOWN BY THE DECREASE IN THE LEVEL OF THE PROTEIN FOLLOWING CASTRATION.  
CC -!- MISCELLANEOUS: C3 IS ENCODED BY TWO DIFFERENT GENES.  
CC -!- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN SUBFAMILY.  
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-----  
EMBL; V01263; CAA24577.1; -;  
DR EMBL; M71245; AAA41965.1; -;  
DR PIR; A03250; BORT3.  
DR InterPro; IPR003627; Mangb/prostatn.  
DR InterPro; IPR000329; Uteroglobln.  
DR Pfam; PF01099; Uteroglobln; 1.  
DR ProDom; PD029354; Mangb/prostatn; 1.  
DR PROSITE; PS00403; UTEROGLOBIN 1; FALSE\_NEG.  
DR PROSITE; PS00404; UTEROGLOBIN 2; 1.  
KW Signal; glycoprotein; steroid-binding.  
FT SIGNAL 1 18  
FT CHAIN 19 95 PROSTATIC STEROID-BINDING PROTEIN C3  
FT CHAIN  
FT CARBOHYD 35 35 N-LINKED (GLCNAC...).  
FT CONFLICT 53 53 D -> A (IN REF. 3).  
FT CONFLICT 79 79 G -> S (IN REF. 2).  
FT SEQUENCE 95 AA; 10730 MW; F7F7F1A0C882E375 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVP 4  
DB 2 KLVP 5  
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RESULT 11  
VNS2\_CVBM STANDARD; PRT; 109 AA.  
ID VNS2\_CVBM  
AC F15774;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Nonstructural protein NS2 (Nonstructural 12.7 kDa protein).  
OS Bovine coronavirus (strain Mebus), and  
OS Bovine coronavirus (strain F15).  
OC Viruses; SERNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=11132, 11129;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mebus;  
RX MEDLINE=90320120; PubMed=2142556;  
RA Abraham S., Kienzie T.E., Lapps W.E., Brian D.A.;  
RT "Sequence and expression analysis of potential nonstructural proteins of 4.9, 4.8, 12.7, and 9.5 kDa encoded between the spike and membrane protein genes of the bovine coronavirus.";  
RT Virology 177:488-495(1990).  
RL [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F15;  
RX MEDLINE=90206809; PubMed=2320429;  
RA Woloszyn N., Boireau P., Laporte J.;  
RT "Nucleotide sequence of the bovine enteric coronavirus BECV F15 mRNA 5 and mRNA 6 unique regions.";  
RL Nucleic Acids Res. 18:1303-1303(1990).  
CC -!- SIMILARITY: 62% TO CORONAVIRUS MHV-JHM NS2.  
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EMBL; X51347; CAA35740.1; -;  
DR EMBL; M31054; AAA42913.1; -;  
DR PIR; S08408; MNH82.  
DR PIR; C46346; C46346.  
KW Nonstructural protein.  
SQ SEQUENCE 109 AA; 12806 MW; 08B7CA339A1BD051 CRC64;  
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Query Match 100.0%; Score 4; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KLVP 4  
DB 89 KLVP 92  
-----  
RESULT 12  
VNS2\_CVHOC STANDARD; PRT; 109 AA.  
ID VNS2\_CVHOC  
AC Q04853;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Nonstructural protein NS2 (Nonstructural 12.9 kDa protein).

```

OS Human coronavirus (strain OC43)..
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=31631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93297129; PubMed=8517026;
RA Mount S., Talbot P.J.;
RT "Human coronavirus OC43 RNA 4 lacks two open reading frames located
RL downstream of the S gene of bovine coronavirus.";
RL Virology 192:355-360(1993).
CC -----
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CC -----
DR EMBL; M99576; AAA02569.1; -.
DR PIR; A44275; A44275.
KM Nonstructural protein.
SQ SEQUENCE 109 AA; 12935 MW; 8F06A6B9B30B1667 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 109;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 89 KLVF 92

RESULT 13
YCX1_CHLRY
ID YCX1_CHLRY STANDARD; PRT; 110 AA.
AC P05720;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 12.7 kDa protein in 16S-23S DNA spacer.
OS Chlorella pyrenoidosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxId=3078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6623262; PubMed=3714498;
RA Yamada T., Shimaji M.;
RT "Peculiar feature of the organization of rRNA genes of the Chlorella
RT chloroplast DNA.";
RL Nucleic Acids Res. 14:3827-3839(1986).
CC -----
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CC -----
DR EMBL; X03846; CAA27477.1; -.
DR PIR; A24444; A24444.
KM Chloroplast; Hypothetical protein.
SQ SEQUENCE 110 AA; 12782 MW; 1F58A6055A1A377 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 110;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 1 KLVF 4

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Db 25 KLVF 28

RESULT 14
FOLB_HAEIN
ID FOLB_HAEIN STANDARD; PRT; 118 AA.
AC P46362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydropyrimidin aldolase (EC 4.1.2.25) (DHNA).
GN FOLB OR H10265.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxId=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spitzgs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: CATALYZES THE CONVERSION OF 7,8-DIHYDROBIOPTERIN TO 6-
CC HYDROXYBIOPTERIN-7,8-DIHYDROBIOPTERIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2-amino-4-hydroxy-6-(D-erythro-1,2,3-
CC trihydroxypropyl)-7,8-dihydropteridine = 2-amino-4-hydroxy-6-
CC hydroxymethyl-7,8-dihydropteridine + glycolaldehyde.
CC -1- PATHWAY: Folate biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE DHNA FAMILY.
CC -----
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CC -----
DR EMBL; U32712; AAC21930.1; -.
DR TIGR; H10265; -.
DR InterPro; IPRO03098; FOLB.
DR Pfam; PF02152; FOLB; 1.
DR TIGRPFAM; TIGR00525; FOLB; 1.
DR TIGRPFAM; TIGR00526; FOLB dom; 1.
KM Lyase; Folate biosynthesis; Complete proteome.
SQ SEQUENCE 118 AA; 13577 MW; 158C716C473DC701 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 118;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 27 KLVF 30

RESULT 15
R22B_YEAST
ID R22B_YEAST STANDARD; PRT; 121 AA.
AC P56628;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

```

```
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S ribosomal protein L22-B.
GN RPL22B OR YFL034BC.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268 (1995).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L22 IN YEAST.
CC -1- SIMILARITY: BELONGS TO THE L22E FAMILY OF RIBOSOMAL PROTEINS.
-----
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-----
DR EMBL; D50617; -; NOT ANNOTATED_CDS.
DR SGD; S0006436; RPL22B.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
DR ProDom; PD007306; Ribosomal_L22e; 1.
DR Ribosomal protein; Multigene family.
KW RIBOSOMAL MET 0
FT INIT MET 0
FT INIT MET 0 BY SIMILARITY
SQ SEQUENCE 121 AA; 13695 MW; 2A0A3EF175C20A26 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4
DB 103 KLVP 106

RESULT 16
FOLB_ECOLI STANDARD; PRT; 122 AA.
AC P31055; P76659;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydropyrimidin aldolase (EC 4.1.2.25) (DHNA).
GN FOLB OR B3058.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=JM83;
RX MEDLINE=93285992; PubMed=8389741;
```

```
RA Cain B.D., Norton P.J., Eubanks W., Nick H.S., Allen C.M.;
RT "Amplification of the bacA gene confers bacitracin resistance to
RT Escherichia coli.";
RL J. Bacteriol. 175:3784-3789 (1993).
RN [3]
RN CHARACTERIZATION.
RX MEDLINE=98516300; PubMed=9651328;
RA Hausmann C., Rohdich F., Schmidt E., Bacher A., Richter G.;
RT "Biosynthesis of pteridines in Escherichia coli. Structural and
RT mechanistic similarity of dihydroneopterin-triphosphate epimerase and
RT dihydroneopterin aldolase.";
RL J. Biol. Chem. 273:17418-17424 (1998).
CC -1- FUNCTION: CATALYZES THE CONVERSION OF 7,8-DIHYDRONEOPTERIN TO 6-
CC HYDROXYMETHYL-7,8-DIHYDROPTERIN. CAN USE L-THREO-DIHYDRONEOPTERIN
CC AND D-ERYTHRO-DIHYDRONEOPTERIN AS SUBSTRATES FOR THE FORMATION OF
CC 6-HYDROXYMETHYLDIHYDROPTERIN, BUT IT CAN ALSO CATALYZE THE
CC EPIMERIZATION OF CARBON 2' OF DIHYDRONEOPTERIN AND
CC DIHYDROMONAPTERIN AT APPRECIABLE VELOCITY.
CC -1- CATALYTIC ACTIVITY: 2-amino-4-hydroxy-6-(D-erythro-1,2,3-
CC trihydroxypropyl)-7,8-dihydropteridine = 2-amino-4-hydroxy-6-
CC hydroxymethyl-7,8-dihydropteridine + glycolaldehyde.
CC -1- PATHWAY: Folate biosynthesis.
CC -1- SUBUNIT: HOMOOCTAMER.
CC -1- SIMILARITY: BELONGS TO THE DHNA FAMILY.
-----
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-----
DR EMBL; U28379; AAA89138.1; ALT INIT.
DR EMBL; AE000387; AAC76094.1; ALT INIT.
DR EMBL; L12966; -; NOT ANNOTATED_CDS.
DR EcoGene; EGI1673; folB.
DR InterPro; IPR003098; FolB.
DR Pfam; PF02152; FolB; 1.
DR TIGRPFAMs; TIGR00525; folB; 1.
DR TIGRPFAMs; TIGR00526; folB dom; 1.
KW Lyase; Folate biosynthesis; Complete proteome.
FT CONFLICT 81 82 EL -> DV (IN REF. 2).
FT CONFLICT 100 122 GAVARAANVGVIIERGNLKENN -> ASGAGGECWRNH
FT (IN REF. 2).
SQ SEQUENCE 122 AA; 13619 MW; BEA82C1E0AA38A55 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVP 4
DB 27 KLVP 30

RESULT 17
CY2_RHOVI STANDARD; PRT; 127 AA.
AC P00083;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome C2 precursor.
GN CYCA.
OS Rhodospseudomonas viridis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Hyphomicrobium group; Blastochloris.
OX NCBI_TaxID=1079;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=DSM 133;
RX MEDLINE=90368560; PubMed=1697576;
```

RA Grishammer R., Wiesner C., Michel H.;  
 RT "Sequence analysis and transcriptional organisation of the  
 RT Rhodospseudomonas viridis cytochrome c2 gene";  
 RL J. Bacteriol. 172:5071-5078(1990).  
 RN [2]  
 RP SEQUENCE OF 21-127.  
 RA MEDLINE=76102814; PubMed=174109;  
 RA Ambler R.P., Meyer T.E., Kamen M.D.;  
 RT "Primary structure determination of two cytochromes c2: close  
 RT similarity to functionally unrelated mitochondrial cytochrome C.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 73:472-475(1976).  
 RN [3]  
 RP REVISION TO 34.  
 RA Ambler R.P.;  
 RL Submitted (JUN-1977) to the PIR data bank.  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RA MEDLINE=95404617; PubMed=674304;  
 RA Sogabe S., Miki M.;  
 RT "Refined crystal structure of ferrocytochrome c2 from  
 RT Rhodospseudomonas viridis at 1.6-A resolution.";  
 RL J. Mol. Biol. 252:235-247(1995).  
 CC -1- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,  
 CC PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR  
 CC TO THE OXIDIZED BACTERIOCHLOROPHYL IN THE PHOTOPHOSPHORYLATION  
 CC PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN  
 CC AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.  
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 CC -----  
 DR EMBL; M59302; AAA26092.1; -;  
 DR PIR; A36720; CCRF2V.  
 DR PDB; 1CRY; 30-APR-94.  
 DR InterPro; IPR000345; Cytc\_heme\_bind.  
 DR InterPro; IPR003088; Cyt\_Ct.  
 DR InterPro; IPR00327; Cyt\_CtAB.  
 DR Pfam; Pf00034; cytochrome\_c/1.  
 DR PRINTS; PR00604; CYTCHRMEDIA.  
 DR Prodom; PD000375; Cyt\_CtAB; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
 KM Electron transport; Photosynthesis; Heme; Signal; 3D-structure.  
 FT SIGNAL 1 20  
 FT CHAIN 1 127  
 FT MOD\_RES 21 21 CYTOCHROME C2.  
 FT BINDING 33 33 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).  
 FT BINDING 36 36 HEME (COVALENT).  
 FT METAL 37 37 HEME (COVALENT).  
 FT METAL 37 37 IRON (HEME AXIAL LIGAND).  
 FT CONFLICT 66 66 IRON (HEME AXIAL LIGAND).  
 FT CONFLICT 104 104 A -> S (IN REF. 2).  
 FT CONFLICT 117 117 V -> I (IN REF. 2).  
 FT CONFLICT 117 117 I -> L (IN REF. 2).  
 FT HELIX 23 29  
 FT TURN 30 30  
 FT HELIX 30 30  
 FT TURN 31 34  
 FT TURN 35 36  
 FT TURN 41 42  
 FT TURN 52 53  
 FT TURN 59 60  
 FT TURN 69 72  
 FT TURN 73 73  
 FT HELIX 80 88  
 FT HELIX 90 92  
 FT TURN 93 93  
 FT TURN 95 96  
 FT TURN 107 116  
 FT HELIX 118 124  
 FT TURN 127 AA; 13665 MM; 398ABCF6A7D0DF4 CRC64;  
 SQ SEQUENCE

Query Match 100.0%; Score 4; DB 1; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 Db 3 KLVF 6  
 RESULT 18  
 ID FAB2\_STREPY STANDARD; PRT; 139 AA.  
 AC P58175;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE (3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (EC 4.2.1.-)  
 DE ((3R)-hydroxymyristoyl ACP dehydratase).  
 GN FABZ OR SPY1746 OR SPY18 1818.  
 OS Streptococcus pyogenes, and  
 OS Streptococcus pyogenes (serotype M18).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314, 186103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Najaf P.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MGAS8232 / Serotype M18;  
 RX MEDLINE=21927593; PubMed=11917108;  
 RA Smoot U.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,  
 RA Sylla G.L., Sturdevant D.E., Ricklefs S.M., Porcelli S.F.,  
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,  
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;  
 RT "Genome sequence and comparative microarray analysis of serotype M18  
 RT group A Streptococcus strains associated with acute rheumatic fever  
 RT outbreaks";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
 CC -1- FUNCTION: INVOLVED IN SATURATED FATTY ACIDS BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE THIOESTER DEHYDRATASE FAMILY.  
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 CC -----  
 DR EMBL; AB006603; AAK34490.1; -;  
 DR EMBL; AB010088; AAL98338.1; -;  
 DR HSSP; P18391; IMKA.  
 DR InterPro; IPR001143; Bac\_Sdehydratase.  
 DR Pfam; PF01377; Thioester\_dehyd; 1.  
 KM Lyase; Lipid synthesis; Lipid A biosynthesis; Complete proteome.  
 FT ACT\_SITE 46 46 BY SIMILARITY.  
 SQ SEQUENCE 139 AA; 15324 MM; 06090333FC20B479 CRC64;  
 QY 1 KLVF 4  
 Query Match 100.0%; Score 4; DB 1; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RN [2]  
 RN SEQUENCE OF 108-146 FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=94075230; PubMed=9253680;  
 RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;  
 RT "A survey of the Mycoplasma genitalium genome by using random  
 RT sequencing.";  
 RL J. Bacteriol. 175:7918-7930(1993).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE EARLY ASSEMBLY PROTEINS OF  
 CC THE 50S RIBOSOMAL SUBUNIT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.  
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 CC -----  
 DR EMBL; U99724; AAC71644.1; -;  
 DR EMBL; U01744; AAD10555.1; -;  
 DR TIGR; MG418; -;  
 DR InterPro: IPR001074; Ribosomal\_L13.  
 DR Pfam: PF00572; Ribosomal\_L13; 1.  
 DR ProDom: PD001791; Ribosomal\_L13; 1.  
 DR TIGRFAMs: TIGR01066; rplM\_bact; 1.  
 DR PROSITE: PS00783; RIBOSOMAL\_L13; 1.  
 KM Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 146 AA; 16667 MW; D2F19B15FA96567A CRC64;

Query Match 100.0%; Score 4; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 102 KLVF 105

RESULT 22  
 M165\_ARATH STANDARD; PRT; 152 AA.  
 ID M165\_ARATH  
 AC Q9C717;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE MLP-like protein 165.  
 GN MLP165 OR AT1G35260 OR T911.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OK NCBI\_TaxID=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Muller S., Klimt S., Hauser M.T.;  
 RT "Molecular and phylogenetic analysis of a gene family in Arabidopsis  
 RT thaliana with similarities to major latex, pathogenesis-related and  
 RT ripening-induced proteins.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler B., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Etgu P., Feldhlym T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,  
 RA Miltsecher J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salberg S.L., Schwartz J.R., Shim P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 408:816-820(2000).  
 CC -1- SIMILARITY: BELONGS TO THE MLP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AJ306144; CAC83582.1; -;  
 DR EMBL; AC069160; AAG51462.1; -;  
 KM Multigene family.  
 SQ SEQUENCE 152 AA; 17841 MW; D20AB62F35BBE1C8 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 DB 56 KLVF 59

RESULT 23  
 NUSB\_FUSNN STANDARD; PRT; 153 AA.  
 ID NUSB\_FUSNN  
 AC OBR11;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE N utilization substance protein B homolog (Nusb protein).  
 GN NUSB OR FN1616.  
 OS Fusobacterium nucleatum (subsp. nucleatum).  
 OC Bacteria; Fusobacteriia; Fusobacterium.  
 OK NCBI\_TaxID=76856;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 25586;  
 RX MEDLINE=2186394; PubMed=1189109;  
 RA Kapralov V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,  
 RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,  
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldman E., Bernal A.,  
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,  
 RA Ponstein M., Kyriides N., Overbeek R.;  
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium  
 RT nucleatum strain ATCC 25586.";  
 RL J. Bacteriol. 184:2005-2018(2002).  
 CC -1- FUNCTION: Involved in the transcription termination process (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE NUSB FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB010469; AAL93731.1; -;



```

KW Transcription termination; Complete proteome.
SQ SEQUENCE 153 AA; 17516 MW; 3DABEBDD82BE898 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 25 KLVF 28

RESULT 24
SPRT HAEIN STANDARD; PRT; 156 AA.
AC P4419;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein sprt homolog.
GN SPRT OR H11173.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus
OC Haemophilus
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512 (1995).
CC -1- SIMILARITY: STRONG, TO E.COLI SPRT.
CC
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CC
CC ENBL; U32797; AAC22826.1; --
DR TIGR; H11173; --
DR InterPro; IPR000130; Zn MTpeptidse.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Zinc; Complete proteome.
FT METAL 65 65 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 66 66 BY SIMILARITY.
FT METAL 69 69 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 156 AA; 18684 MW; BBEF66F0585C465A CRC64;

Query Match 100.0%; Score 4; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 148 KLVF 151

RESULT 25
FLGA_AGR75 STANDARD; PRT; 162 AA.
ID FLGA_AGR75
```

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AC Q44339;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Flagellar protein flga precursor.
GN FLGA OR ATU0551 OR AGR C.971.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305158; PubMed=9161424;
RA Deakin W.J., Furniss C.S., Parker V.E., Shaw C.H.;
RT "Isolation and characterisation of a linked cluster of genes from
RT Agrobacterium tumefaciens encoding proteins involved in flagellar
RT basal-body structure.";
RL Gene 189:135-137 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
RL Science 294:2317-2323 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Houmlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlo K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
CC -1- SIMILARITY: TO R.NELIOTI FLGA.
CC
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CC
CC ENBL; U39941; AAB68969.1; --
DR ENBL; U95165; AAB71791.1; --
DR ENBL; A8009024; AAL41568.1; --
DR ENBL; A8009024; AAL41568.1; --
DR InterPro; IPR004924; FLGA.
DR Pfam; PF03240; FLGA; 1.
KW Flagella; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 26 POTENTIAL
FT CHAIN 27 162 FLAGELLAR PROTEIN FLGA.
SQ SEQUENCE 162 AA; 16991 MW; 47B325319552A0A8 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KLVF 4  
 DB 110 KLVF 113

RESULT 26  
 ID RLI0\_HELPJ STANDARD; PRT; 164 AA.  
 AC O92K22;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein L10.  
 GN RPLJ OR HPI123.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 CC Helicobacter.  
 NC NCB1\_TaxID=85963;  
 OK NCB1\_TaxID=85963;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
 RA Thummler P.J., Caruso A., Ulla-Nickelsen M., Mills D.W., Ives C.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori."  
 RL Nature 397:176-180(1999).  
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; AEO01540; AAD06701.1; -  
 DR InterPro; IPR001790; Ribosomal\_L10.  
 DR InterPro; IPR002363; Ribosomal\_L10eub.  
 DR Pfam; PF00466; Ribosomal\_L10; 1.  
 DR PROSITE; PS01109; RIBOSOMAL\_L10; 1.  
 KM Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 164 AA; 18573 MW; E307C2448B5F17F6 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 DB 93 KLVF 96

RESULT 27  
 ID RLI0\_HELPJ STANDARD; PRT; 164 AA.  
 AC P56036;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein L10.  
 GN RPLJ OR HPI1200.  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 CC Helicobacter.  
 NC NCB1\_TaxID=210;  
 OK NCB1\_TaxID=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=26695 / ATCC 700392;  
 RX MEDLINE=97394467; PubMed=9252185;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,  
 RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,  
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,  
 RA Loftus B., Richardson D., Dodson R., Khaila H.G., Glodok A.,  
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,  
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,  
 RA Cotton M.D., Meldrum J.M., Fujii C., Bowman C., Wathey L., Wallin E.,  
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the gastric pathogen Helicobacter  
 RT pylori."  
 RL Nature 388:539-547(1997).  
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
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DR EMBL; AEO00626; AAD08246.1; -  
 DR TIGR; HPI200; -  
 DR InterPro; IPR001790; Ribosomal\_L10.  
 DR InterPro; IPR002363; Ribosomal\_L10eub.  
 DR Pfam; PF00466; Ribosomal\_L10; 1.  
 DR PROSITE; PS01109; RIBOSOMAL\_L10; 1.  
 KM Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 164 AA; 18605 MW; 9915415D78AF5D97 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 DB 93 KLVF 96

RESULT 28  
 ID BAIE\_EUBSP STANDARD; PRT; 166 AA.  
 AC P19412;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Bile acid-inducible operon protein E.  
 GN BAIE.  
 OS Escherichia coli (strain VPI 12708).  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 NC NCB1\_TaxID=29347;  
 OK NCB1\_TaxID=29347;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-31.  
 RX MEDLINE=91072253; PubMed=2254270;  
 RA Mallonee D.H., White W.B., Hylemon P.B.;  
 RT "Cloning and sequencing of a bile acid-inducible operon from  
 RT Escherichia coli strain VPI 12708."  
 RL J. Bacteriol. 172:7011-7019(1990).  
 CC -1- PATHWAY: Bile acid catabolism.  
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DR EMBL; U57489; AAC45413.1; -  
 DR PIR; D37844; D37844.  
 KM Bile acid catabolism.

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FT CONFLICT 2 2 T -> F (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 166 AA; 19533 MW; 1CBCE86C85ADC3B5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 166;
Matches 4; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 KLVF 4
Db 58 KLVF 61

RESULT 29
PMPA CANBO
ID PMPA CANBO STANDARD; PRT; 166 AA.
AC P14292;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Peroxisomal membrane protein A (PMP20).
GN PMPA.
OS Candida boidinii (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5477;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-25.
RC STRAIN=ATCC 32119;
RX MEDLINE=89340488; PubMed=2760051;
RA Garrard L.J., Goodman J.M.;
RT "Two genes encode the major membrane-associated protein of methanol-
induced peroxisomes from Candida boidinii."
RL J. Biol. Chem. 264:13929-13937(1989).
RN [2]
CROSS-REACTIVITY WITH ASP F 3.
RX MEDLINE=98074056; PubMed=9412580;
RA Hennam S., Blaser K., Cramer R.;
RT "Allergens of Aspergillus fumigatus and Candida boidinii share IgE-
binding epitopes."
RL Am. J. Respir. Crit. Care Med. 156:1956-1962(1997).
CC -1- FUNCTION: ITS FUNCTION IS VERY LIKELY TO BE RELATED TO THE
METABOLISM OF METHANOL.
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL; MEMBRANE-ASSOCIATED.
CC -1- INDUCTION: BY METHANOL.
CC -1- MISCELLANEOUS: SHARE COMMON IGE-BINDING EPITOPES WITH ALLERGEN ASP
F 3 OF ASPERGILLUS FUMIGATUS.
CC -1- SIMILARITY: BELONGS TO THE PEROXIREDOXIN 2 FAMILY.
CC -----
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CC -----
CC EMBL; J04984; AAA34357.1; -
CC PIR; A32646; A32646.
CC HSP; P30044; 1HD2.
CC InterPro; IPR008866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
CC PROSITE; PS00342; MICROBODIES CTER; 1.
KW Methanol utilization; Membrane; Peroxisome; Multigene family.
FT INIT_MET 0
FT SITE_164 166 MICROBODY TARGETING SIGNAL.
FT SEQUENCE 166 AA; 17873 MW; CRA078112FBD62A CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 166;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 58 KLVF 61

RESULT 30
YBGA ECOLI
ID YBGA ECOLI STANDARD; PRT; 169 AA.
AC P24252;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein ybga (TKP) (ORF169).
GN YBGA OR B0707.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=84185763; PubMed=6325460;
RA Sancar G.B., Smith F.W., Lorence M.C., Rupert C.S., Sancar A.;
RT "Sequences of the Escherichia coli photolyase gene and protein."
RL J. Biol. Chem. 259:6033-6038(1984).
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=KL2 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shaoy Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1233-1238(1997).
RN [3]
SEQUENCE FROM N.A.
RX STRAIN=KL2;
RX MEDLINE=97061202; PubMed=8905232;
RA Ohnita T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 7.18-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
RN [4]
SEQUENCE OF 1-115 FROM N.A.
RX STRAIN=KL2;
RX MEDLINE=93259920; PubMed=8387990;
RA Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;
RT "Rhs elements of Escherichia coli K-12: complex composites of shared
and unique components that have different evolutionary histories."
RL J. Bacteriol. 175:2799-2808(1993).
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CC -----
CC EMBL; K01299; AAA34387.1; -
CC EMBL; AE000174; AAC73801.1; -
CC EMBL; D90709; BAA35366.1; -
CC EMBL; D90710; BAA35371.1; -
CC EMBL; L02373; AAC63077.1; -
CC EMBL; EGI108; ybga.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 169 AA; 20211 MW; 32BA716EB3FB5C53 CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 1; Length 169;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KLVF 4  
 ||||  
 Db 41 KLVF 44

RESULT 31  
 V6B\_CVFE3 STANDARD; PRT; 176 AA.

AC P33467;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Protein 6B.  
 OS Feline enteric coronavirus (strain 79-1683).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage, Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 NC NCB1\_TaxID=33733;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93033103; PubMed=1329312;  
 RA Venema H., Roosen J.W.A., Wesseling J., Horzinek M.C.,  
 RA Rottler P.J.M.;  
 RT "Genomic organization and expression of the 3' end of the canine and  
 RT feline enteric coronaviruses.";  
 RL Virology 191:134-140(1992).

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CC  
 CC EMBL; X66718; CAA47250.1; -.  
 DR PIR; B44056; E44056.  
 DR InterPro; IPR004945; Corona\_6B\_7B.  
 DR Pfam; PF03262; Corona\_6B\_7B\_1.  
 SQ SEQUENCE 176 AA; 20205 MM; 4AC8B9811C8DB440 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 134 KLVF 137

RESULT 32  
 TAGL\_BOVIN STANDARD; PRT; 180 AA.

AC Q9T887;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Transgelin (Smooth muscle protein 22-alpha) (SM22-alpha) (25 kDa F-  
 DE actin-binding protein) (Fragment).  
 GN TAGLN OR SM22.

OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NC NCB1\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Arteria;  
 RX MEDLINE=94161744; PubMed=8117285;  
 RA Kobayashi R., Kubota T., Hidaka H.;  
 RT "Purification, characterization, and partial sequence analysis of a  
 RT new 25-kDa actin-binding protein from bovine aorta: a SM22 homolog.";

RL Biochem. Biophys. Res. Commun. 198:1275-1280(1994).  
 CC -1- FUNCTION: ACTIN CROSS-LINKING/GELING PROTEIN (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -1- INDUCTION: BY GROWTH FACTORS.  
 CC -1- SIMILARITY: BELONGS TO THE CALPONIN FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.

DR InterPro; IPR003247; CH\_type.  
 DR InterPro; IPR001715; Calponin-like.  
 DR InterPro; IPR000557; Calponin repeat.  
 DR InterPro; IPR003096; SM22\_calponin.  
 DR Pfam; PF00307; CH\_1.  
 DR Pfam; PF00402; calponin; 1.  
 DR PRINTS; PR00888; SM22CALPONIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR SMART; SM00033; CH\_1.  
 DR PROSITE; PS01052; CALPONIN; 1.  
 DR PROSITE; PSS0021; CH; 1.  
 KW Muscle protein.  
 FT DOMAIN 1 117 CH.  
 FT REPEAT 155 180 CALPONIN-LIKE 26 AA MOTIF.  
 FT NON\_TER 180 180  
 SQ SEQUENCE 180 AA; 20327 MM; DC5C1667181D66A CRC64;

Query Match 100.0%; Score 4; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 ||||  
 Db 44 KLVF 47

RESULT 33  
 ITRB\_SOYBN STANDARD; PRT; 181 AA.

AC P01071;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Trypsin inhibitor B (Kunitz).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 NC NCB1\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=CV. NORIN NO. 2;  
 RX MEDLINE=86059307; PubMed=3905784;  
 RA Kim S.-H., Hara S., Hase S., Ikenaka T., Toda H., Kitamura K.,  
 RA Kaizuma N.;  
 RT "Comparative study on amino acid sequences of Kunitz-type soybean  
 RT trypsin inhibitors, Tia, T1b, and T1c.";  
 RL J. Biochem. 98:435-448(1985).

CC -1- FUNCTION: INHIBITION OF TRYPSIN.  
 CC -1- MISCELLANEOUS: ELECTROPHORESIS IDENTIFIES THREE GENETICALLY  
 CC DISTINCT VARIANTS, A, B, AND C, THAT ARE INHERITED AS CODOMINANT  
 CC ALLELES.

CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR  
 CC FAMILY.

DR PIR; A01310; TISVB.  
 DR HSSP; P01070; IAWV.  
 DR InterPro; IPR002160; Kunitz\_legume.  
 DR Pfam; PF00197; Kunitz\_legume; 1.  
 DR PRINTS; PR00291; KUNITZINHBR.  
 DR ProDom; PD000891; Kunitz\_legume; 1.  
 DR SMART; SM00452; STI; 1.  
 DR PROSITE; PS00283; SOYBEAN KUNITZ; 1.

KW Serine protease inhibitor.  
 FT ACT\_SITE 63 64 REACTIVE BOND (TRYPSIN).  
 FT DISULFID 39 86 BY SIMILARITY.  
 FT DISULFID 136 145 BY SIMILARITY.

SQ SEQUENCE 181 AA; 20040 MW; C134E9891866C787 CRC64;  
Query Match 100.0%; Score 4; DB 1; Length 181;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 132 KLVF 135

RESULT 34  
ATPD CYAPA STANDARD; PRT; 186 AA.  
AC P48082;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE ATP synthase delta chain (EC 3.6.3.14).  
GN ATPD.  
OS Cyanophora paradoxa.  
OC Cyanelle.  
OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.  
OX NCBI\_TaxID=2762;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LB555 / Pringsheim;  
RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,  
RA Bryant D.A.;  
RT Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.;  
RL Plant Mol. Biol. Rep. 13:327-332(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LB555 / Pringsheim;  
RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,  
RA Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,  
RA Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;  
RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:  
the genetic complexity of a primitive plastid."  
RL (in) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,  
RL Schwenmler W. (eds.);  
RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg  
RL (1997).  
CC -!- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS  
CC CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANGES FROM  
CC CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.  
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
CC H(+) (out).  
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC  
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE  
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
CC HAS THREE MAIN SUBUNITS: A, B AND C.  
CC -!- SUBCELLULAR LOCATION: CYANELLE THYLAKOID MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.  
CC  
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CC  
CC EMBL: U30821; AAA81254.1; --  
CC InterPro: IPR000711; ATPsynth\_OSCP.  
CC Pfam: PF00213; OSCP; 1  
CC PRINTS: PR00125; ATPASEDELTA.  
CC TIGRFAMs: TIGR01145; ATP\_synth\_delta; 1.  
CC PROSITE: PS00389; ATPASE\_DELTA; 1.  
CC KW Hydroxylase; ATP synthetase; CF(1); Cyanelle; Hydrogen ion transport.  
SQ SEQUENCE 186 AA; 20767 MW; D6397872F9543D1C CRC64;  
Query Match 100.0%; Score 4; DB 1; Length 186;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 144 KLVF 147

RESULT 35  
YBAY ECOLI STANDARD; PRT; 190 AA.  
AC P77717;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ybay precursor.  
DE Hypothetical protein ybay precursor.  
GN YBAY OR B0453.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12."  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,  
RA Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,  
RA Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
CC (Probable).  
CC  
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CC  
CC EMBL: AB000151; AAC73556.1; --  
CC EMBL: U82664; AAB40209.1; --  
CC DR ECoGene; EG13253; YBAY.  
CC DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.  
CC KW Hypothetical protein; Lipoprotein; Membrane; Signal;  
CC Complete proteome.  
CC FT SIGNAL 1 18 POTENTIAL.  
CC FT CHAIN 19 190 HYPOTHETICAL LIPOPROTEIN YBAY.  
CC FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
SQ SEQUENCE 190 AA; 19431 MW; 1684A26AD05EF68D CRC64;  
Query Match 100.0%; Score 4; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 127 KLVF 130

RESULT 36  
TERR ALICSP STANDARD; PRT; 191 AA.  
AC P187B2;  
DT 01-NOV-1990 (Rel. 16, Created)

```

DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tellurium resistance protein tere.
GN TERE.
OS Alcaligenes sp.
OC Plasmid IncHI2 pMER610.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Alcaligenes.
OX NCBI_TaxId=512;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006266; PubMed=3049247;
RA Jobling M.G., Ritchie D.A.;
RT "The nucleotide sequence of a plasmid determinant for resistance to
telurium anions."
RL Gene 66:245-258(1988).
CC -1- FUNCTION: NOT KNOWN; SEEM TO CONTRIBUTE TO THE TELLURIUM (TER)
RESISTANCE MECHANISM.
CC -1- SIMILARITY: BELONGS TO THE CAPAB / TERDEXZ FAMILY.
CC -----
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CC -----
DR EMBL; M20238; AAA98293.1; -
DR PIR; E30754; E30754.
DR InterPro; IPR003325; TereD.
DR Pfam; PF02342; TereD; 1.
DR Tellurium resistance; Plasmid.
SQ SEQUENCE 191 AA; 20415 MW; 5CE11C58B31447F2 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 104 KLVF 107

RESULT 37
TERE SERMA
ID TERE SERMA STANDARD; PRT; 191 AA.
AC 052358;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tellurium resistance protein tere.
GN TERE.
OS Serratia marcescens.
OC Plasmid IncHI2 R478.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxId=615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95394806; PubMed=7665479;
RA Whelan K.F., Collieran E., Taylor D.E.;
RT "Phage inhibition, colicin resistance, and tellurite resistance are
encoded by a single cluster of genes on the IncHI2 plasmid R478."
RL J. Bacteriol. 177:5016-5027(1995).
CC -1- FUNCTION: NOT KNOWN; SEEM TO CONTRIBUTE TO THE TELLURIUM (TER)
RESISTANCE MECHANISM. ALSO INVOLVED IN PHAGE INHIBITION (PHI) AND
COLICIN RESISTANCE (PACB).
CC -1- SIMILARITY: BELONGS TO THE CAPAB / TERDEXZ FAMILY.
CC -----
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CC -----
DR EMBL; U59239; AAA68851.1; -
DR InterPro; IPR003325; TereD.
DR Pfam; PF02342; TereD; 1.
DR Tellurium resistance; Plasmid.
SQ SEQUENCE 191 AA; 20448 MW; EF9BA85947BE2767 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4
Db 104 KLVF 107

RESULT 38
Y611 META
ID Y611 META STANDARD; PRT; 191 AA.
AC 058028;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJO611.
GN MJO611.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxId=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bait C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake O., Olsen G.J., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Retch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Utermack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
RT "complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL; U67509; AAB98604.1; -
DR TIGR; MJO611; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 110 130 POTENTIAL.
FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 171 191 POTENTIAL.
SQ SEQUENCE 191 AA; 21834 MW; 0F613A043DEFTDA9 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4

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```
Db      80 KLVF 83
|||||
RESULT 39
DVR_BPT4
ID_DVR_BPT4 STANDARD; PRT; 193 AA.
AC P04382;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydrofolate reductase (EC 1.5.1.3).
GN FRD.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=84212439; PubMed=6327673;
RA Purohit S., Mathews C.K.;
RT "Nucleotide sequence reveals overlap between T4 phage genes encoding
RT dihydrofolate reductase and thymidylate synthase.";
RL J. Biol. Chem. 259:6261-6266(1984).
RN [2]
SEQUENCE FROM N.A.
RP Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE OF 123-193 FROM N.A.
RP STRAIN=ALC4;
RC MEDLINE=86189927; PubMed=3698096;
RA Chu F.K., Maley G.F., West D.K., Belfort M., Maley F.;
RT "Characterization of the intron in the phase T4 thymidylate synthase
RT gene and evidence for its self-excision from the primary
RT transcript.";
RL Cell 45:157-166(1986).
CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-
CC dihydrofolate + NADPH.
CC -1- PATHWAY: ESSENTIAL STEP FOR DE NOVO GLYCINE AND PURINE SYNTHESIS,
CC DNA PRECURSOR SYNTHESIS, AND FOR THE CONVERSION OF DUMP TO DTMP.
CC -1- SIMILARITY: BELONGS TO THE DIHYDROFOLATE REDUCTASE FAMILY.
-----
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-----
DR EMBL; K01804; AAA32491.1; -.
DR EMBL; AF158101; AAD42577.1; -.
DR EMBL; M12742; AAC12815.1; -.
DR PIR; A00396; RDBPT4.
DR InterPro; IPR001796; DHFR.
DR Pfam; PF00186; Dihfolate_red; 1.
DR PRINTS; PR00070; DHFR.
DR PROSITE; PS00075; DHFR; 1.
KW Oxidoreductase; NADP; Trimethoprim resistance;
KW Methotrexate resistance; One-carbon metabolism.
SQ SEQUENCE 193 AA; 21713 MW; 64E033916E628178 CRC64;
Query Match 100.0%; Score 4; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVF 4
|||
Db 3 KLVF 6
```

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RESULT 40
SAR1_CAEEL STANDARD; PRT; 193 AA.
ID SAR1_CAEEL
AC Q23475;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP-binding protein SAR1.
GN ZK180.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Pauley A., Le T.T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN TRANSPORT FROM THE ENDOPLASMIC RETICULUM
CC TO THE GOLGI APPARATUS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. SAR1 FAMILY.
-----
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-----
DR EMBL; U58748; AAB52968.1; -.
DR HSSP; P32889; LRRG.
DR WormPep; ZK180.4; CE07622.
DR InterPro; IPR000251; ARF family.
DR InterPro; IPR002046; Sar1_GTPBP.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00025; arf; 1.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01020; SAR1; 1.
KW GTP-binding; Protein transport; Endoplasmic reticulum; Golgi stack.
FT NP_BIND 28 35 GTP (BY SIMILARITY).
FT NP_BIND 71 74 GTP (BY SIMILARITY).
FT NP_BIND 130 133 GTP (BY SIMILARITY).
SQ SEQUENCE 193 AA; 21709 MW; 03E76FD1EC163C5F CRC64;
Query Match 100.0%; Score 4; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLVF 4
|||
Db 23 KLVF 26
```

Search completed: January 3, 2003, 07:52:19  
Job time : 33 secs

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OM protein - protein search, using sw model

Run on: January 3, 2003, 07:47:51 ; Search time 29 Seconds  
(without alignments)  
28.420 Million cell updates/sec

Title: US-09-867-847-15

Perfect score: 4

Sequence: 1 KLVF 4

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

SPTREMBL 21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	100.0	14	Q9UH91	Q9uh91 homo sapien
2	4	100.0	19	Q9UCC8	Q9ucc8 homo sapien
3	4	100.0	27	Q9UWG8	Q9uwg8 thermococu
4	4	100.0	28	Q9UCD1	Q9ucd1 homo sapien
5	4	100.0	30	Q9UCA9	Q9uca9 homo sapien
6	4	100.0	33	Q9UC33	Q9uc33 homo sapien
7	4	100.0	47	Q52455	Q52455 pyrococcus
8	4	100.0	48	Q9GR26	Q9gr26 aphididus co
9	4	100.0	51	Q8QMN2	Q8qmn2 compox viru
10	4	100.0	52	Q9MEH0	Q9meh0 meganactiph
11	4	100.0	54	Q8RBV2	Q8rbv2 thermosaeer
12	4	100.0	57	Q921T0	Q921t0 rickettsia
13	4	100.0	58	Q39633	Q39633 calicivirus
14	4	100.0	61	Q9ATZ0	Q9atz0 shigella fl
15	4	100.0	62	Q8W6C9	Q8w6c9 vibrio phag
16	4	100.0	63	Q8SPJ7	Q8spj7 sus scrofa

17	4	100.0	64	Q9NHV7	Q9nhv7 drosophila
18	4	100.0	65	Q94144	Q94144 caenorhabdi
19	4	100.0	67	Q921F4	Q921f4 rickettsia
20	4	100.0	69	Q9SMP2	Q9smp2 arabidopsis
21	4	100.0	71	Q8UC16	Q8uc16 agrobacteri
22	4	100.0	72	Q25925	Q25925 plasmodium
23	4	100.0	74	Q936G7	Q936g7 staphylococ
24	4	100.0	76	Q8VVM4	Q8vvm4 escherichia
25	4	100.0	76	Q9TBS6	Q9tbs6 toxostoma l
26	4	100.0	76	Q9TBS2	Q9tbs2 toxostoma r
27	4	100.0	77	Q54879	Q54879 streptococ
28	4	100.0	78	Q9HPR1	Q9hpr1 halobacteri
29	4	100.0	79	Q969F3	Q969f3 homo sapien
30	4	100.0	79	Q35463	Q35463 cricetus
31	4	100.0	79	Q92GT7	Q92gt7 rickettsia
32	4	100.0	81	Q96183	Q96183 plasmodium
33	4	100.0	82	Q16014	Q16014 homo sapien
34	4	100.0	82	Q16019	Q16019 homo sapien
35	4	100.0	82	Q16020	Q16020 homo sapien
36	4	100.0	82	P78438	P78438 homo sapien
37	4	100.0	83	Q8UC93	Q8uc93 agrobacteri
38	4	100.0	84	Q8YH11	Q8yh11 bruceella me
39	4	100.0	85	Q9TBS4	Q9tbs4 toxostoma g
40	4	100.0	85	Q9TBS0	Q9tbs0 toxostoma o
41	4	100.0	85	Q9TBR8	Q9tbr8 toxostoma c
42	4	100.0	85	Q9TBR6	Q9tbr6 toxostoma c
43	4	100.0	85	Q9TBR4	Q9tbr4 oreoscoptes
44	4	100.0	85	Q9TBR2	Q9tbr2 toxostoma b
45	4	100.0	85	Q9TBR0	Q9tbr0 toxostoma c
46	4	100.0	85	Q9TBR8	Q9tbr8 toxostoma r
47	4	100.0	85	Q9TBO7	Q9tbo7 toxostoma l
48	4	100.0	85	Q9TBO6	Q9tbo6 toxostoma l
49	4	100.0	85	Q9BAC8	Q9bac8 rhizobium l
50	4	100.0	90	Q9B8C5	Q9b8c5 toxostoma c
51	4	100.0	90	Q9PF74	Q9pf74 xyliella fas
52	4	100.0	90	Q9HMB9	Q9hmb9 halobacteri
53	4	100.0	91	Q92HJ5	Q92hj5 rickettsia
54	4	100.0	92	Q29222	Q29222 sus scrofa
55	4	100.0	92	Q8W306	Q8w306 silene conl
56	4	100.0	93	Q9B8C4	Q9b8c4 toxostoma c
57	4	100.0	94	Q9B8C7	Q9b8c7 toxostoma c
58	4	100.0	94	Q9B8Y0	Q9b8y0 toxostoma c
59	4	100.0	94	Q9B866	Q9b866 malawimonas
60	4	100.0	95	Q9B116	Q9b116 toxostoma c
61	4	100.0	95	Q9B8C6	Q9b8c6 toxostoma c
62	4	100.0	95	Q9B8B5	Q9b8b5 toxostoma c
63	4	100.0	95	Q976D1	Q976d1 rattus norv
64	4	100.0	96	Q22664	Q22664 caenorhabdi
65	4	100.0	96	Q9G1S2	Q9g1s2 toxostoma c
66	4	100.0	96	Q9G1N2	Q9g1n2 toxostoma c
67	4	100.0	96	Q9G8Y8	Q9g8y8 toxostoma r
68	4	100.0	96	Q9G8Y7	Q9g8y7 toxostoma b
69	4	100.0	96	Q9G8Y6	Q9g8y6 toxostoma c
70	4	100.0	96	Q9G8Y5	Q9g8y5 toxostoma c
71	4	100.0	96	Q9G8Y4	Q9g8y4 toxostoma c
72	4	100.0	96	Q9G8Y3	Q9g8y3 toxostoma c
73	4	100.0	96	Q9G8Y2	Q9g8y2 toxostoma c
74	4	100.0	96	Q9G8Y1	Q9g8y1 toxostoma c
75	4	100.0	96	Q9G8X9	Q9g8x9 toxostoma c
76	4	100.0	96	Q9G8E5	Q9g8e5 sheppardia
77	4	100.0	96	Q9G8E4	Q9g8e4 sheppardia
78	4	100.0	97	Q13778	Q13778 homo sapien
79	4	100.0	97	Q9ZL00	Q9zl00 helicobacte
80	4	100.0	97	Q25361	Q25361 helicobacte
81	4	100.0	98	Q9MYT1	Q9myt1 oryctolagus
82	4	100.0	99	Q14371	Q14371 schizosacch
83	4	100.0	99	Q9G148	Q9g148 sheppardia
84	4	100.0	99	Q94EWS	Q94ews arabidopsis
85	4	100.0	99	Q8VAV7	Q8vav7 white spot
86	4	100.0	99	Q97S58	Q97s58 streptococ
87	4	100.0	100	Q9G8D5	Q9g8d5 sheppardia
88	4	100.0	100	Q9G8D4	Q9g8d4 sheppardia
89	4	100.0	100	Q9KCS5	Q9kcs5 bacillus ha

90	4	100.0	100	16	Q825D9	Q8z5d9 salmonella	163	4	100.0	135	10	Q9S760	Q9s760 arabisopsis
91	4	100.0	101	4	Q9BZ77	Q9bz77 homo sapien	164	4	100.0	135	16	Q93JB3	Q93jb3 streptomyc
92	4	100.0	101	8	Q47595	O47595 polioptilla	165	4	100.0	136	9	Q8SCL9	Q8scl9 pseudomonas
93	4	100.0	101	8	Q47596	O47596 polioptilla	166	4	100.0	136	10	Q9SXI7	Q9sxi7 youngia jap
94	4	100.0	101	8	Q48282	O48282 polioptilla	167	4	100.0	136	16	Q9CND9	Q9cnd9 pasteurella
95	4	100.0	101	8	Q48326	O48326 polioptilla	168	4	100.0	136	17	Q97ZA3	Q97za3 sulfolobus
96	4	100.0	101	8	Q48354	O48354 polioptilla	169	4	100.0	138	2	P94Z97	P94z97 bacillus ps
97	4	100.0	101	16	Q928G1	Q928g1 listeria in	170	4	100.0	139	2	Q53856	Q53856 spiroplasma
98	4	100.0	102	8	Q9G8U6	Q9g8u6 rhodomonas	171	4	100.0	139	16	Q67435	Q67435 aquifex aeo
99	4	100.0	103	17	Q972A6	Q972a6 sulfolobus	172	4	100.0	140	2	Q9AFQ7	Q9afq7 shigella fl
100	4	100.0	105	3	Q9C110	Q9c110 schizosacch	173	4	100.0	140	11	Q99MT5	Q99mt5 mus musculu
101	4	100.0	105	5	Q9TV71	Q9tv71 plasmodium	174	4	100.0	140	11	Q63500	Q63500 rattus norv
102	4	100.0	105	16	Q983W8	Q983w8 rhizobium l	175	4	100.0	142	11	Q97NJ8	Q97nj8 streptococc
103	4	100.0	106	12	Q69580	Q69580 human herpe	176	4	100.0	142	17	Q9V0B5	Q9vob5 pyrococcus
104	4	100.0	107	10	Q99UE9	Q99ue9 arabisopsis	177	4	100.0	144	16	Q8YJW1	Q8yjlw1 anabaena sp
105	4	100.0	107	16	Q9CEB7	Q9ceb7 lactococcus	178	4	100.0	146	5	Q96438	Q96438 crithidia f
106	4	100.0	109	12	Q84732	Q84732 porcine hem	179	4	100.0	146	16	Q8YR30	Q8yr30 anabaena sp
107	4	100.0	109	12	Q9QAQ5	Q9qaq5 bovine coro	180	4	100.0	146	17	Q97AX5	Q97ax5 thermoplas
108	4	100.0	109	12	Q99H66	Q99h66 bovine coro	181	4	100.0	147	16	Q55533	Q55533 synechocyst
109	4	100.0	109	12	Q9DR78	Q9dr78 bovine coro	182	4	100.0	148	10	Q8S991	Q8s991 polygonum h
110	4	100.0	110	12	Q8V434	Q8v434 bovine coro	183	4	100.0	148	16	Q98LE5	Q98le5 rhizobium l
111	4	100.0	109	12	Q89792	Q89792 porcine hem	184	4	100.0	150	10	Q91J79	Q91j79 arabisopsis
112	4	100.0	109	12	Q9PY31	Q9py31 bovine coro	185	4	100.0	150	12	Q8QUQ8	Q8quq8 infectious
113	4	100.0	109	12	Q9QAR2	Q9qar2 bovine coro	186	4	100.0	152	2	Q9ALY1	Q9aly1 carsonella
114	4	100.0	109	16	Q8ZN62	Q8zn62 salmonella	187	4	100.0	152	10	Q9STZ9	Q9stz9 arabisopsis
115	4	100.0	109	17	Q8ZX86	Q8zx86 pyrobaculum	188	4	100.0	153	11	Q9D5X0	Q9d5x0 mus musculu
116	4	100.0	109	17	Q8U2J2	Q8u2j2 pyrococcus	189	4	100.0	153	16	Q8RII1	Q8rii1 fusobacteri
117	4	100.0	110	10	Q94CG2	Q94cg2 arabisopsis	190	4	100.0	154	12	Q91C38	Q91c38 hepatitis b
118	4	100.0	110	16	Q8YQZ5	Q8yqz5 anabaena sp	191	4	100.0	155	12	Q9WHX5	Q9whx5 tomato gold
119	4	100.0	110	17	Q96ZJ0	Q96zj0 sulfolobus	192	4	100.0	157	2	Q85802	Q85802 salmonella
120	4	100.0	112	1	P95858	P95858 sulfolobus	193	4	100.0	157	2	Q92488	Q92488 aeromonas s
121	4	100.0	112	10	Q9M296	Q9m296 arabisopsis	194	4	100.0	157	2	Q934B2	Q934b2 escherichia
122	4	100.0	116	2	Q53750	Q53750 ataphylococ	195	4	100.0	157	5	Q9W1J7	Q9w1j7 drosophila
123	4	100.0	116	2	Q934S7	Q934s7 thibacillu	196	4	100.0	157	16	Q8UHX2	Q8uhx2 agrobacteri
124	4	100.0	116	10	Q9FED2	Q9fed2 arabisopsis	197	4	100.0	158	9	Q8SCG0	Q8scg0 vibrio harv
125	4	100.0	116	10	Q9SW30	Q9sw30 arabisopsis	198	4	100.0	158	10	Q9SYL3	Q9syl3 arabisopsis
126	4	100.0	116	16	Q9WXT9	Q9wxt9 thermotoga	199	4	100.0	158	16	Q92825	Q92825 rhizobium m
127	4	100.0	116	16	Q8XZB9	Q8xzb9 escherichia	200	4	100.0	159	16	Q85816	Q85816 helicobacte
128	4	100.0	116	17	Q8TWS7	Q8tws7 methanopyru	201	4	100.0	159	16	Q92K08	Q92k08 helicobacte
129	4	100.0	117	9	O03932	O03932 bacterioph	202	4	100.0	159	16	Q9HZR2	Q9hzz2 pseudomonas
130	4	100.0	117	10	O23494	O23494 arabisopsis	203	4	100.0	159	16	Q98DG0	Q98dg0 rhizobium l
131	4	100.0	118	2	Q9EVX0	Q9evx0 streptococc	204	4	100.0	159	16	Q928Q1	Q928q1 listeria in
132	4	100.0	118	16	Q9CKC6	Q9ckc6 pasteurella	205	4	100.0	159	16	Q8Y4Q2	Q8y4q2 listeria mo
133	4	100.0	119	5	Q95YG4	Q95yg4 caenorhabdi	206	4	100.0	160	9	Q64368	Q64368 lactobacill
134	4	100.0	119	16	Q8Z166	Q8zi66 yersinia pe	207	4	100.0	160	16	Q92EN8	Q92en8 listeria in
135	4	100.0	120	10	P93251	P93251 musa acumin	208	4	100.0	160	16	Q929U3	Q929u3 bacillus ha
136	4	100.0	120	10	Q8SAA7	Q8saa7 oryza sativ	209	4	100.0	161	12	Q91719	Q91719 measles vir
137	4	100.0	120	16	Q8ZLY2	Q8zly2 salmonella	210	4	100.0	161	12	O11720	O11720 measles vir
138	4	100.0	120	16	Q8Z3M7	Q8z3m7 salmonella	211	4	100.0	161	12	O11721	O11721 measles vir
139	4	100.0	121	2	Q9F440	Q9f440 escherichia	212	4	100.0	161	12	O11722	O11722 measles vir
140	4	100.0	121	2	Q93PW9	Q93pw9 shigella so	213	4	100.0	161	12	O11723	O11723 measles vir
141	4	100.0	121	2	Q93GK0	Q93gk0 bacillus st	214	4	100.0	161	12	O11724	O11724 measles vir
142	4	100.0	122	2	Q49928	Q49928 mycobacteri	215	4	100.0	161	12	O11725	O11725 measles vir
143	4	100.0	122	16	Q9K5Q1	Q9k5q1 bacillus ha	216	4	100.0	161	12	O11726	O11726 measles vir
144	4	100.0	122	16	Q8Y239	Q8y239 anabaena sp	217	4	100.0	161	12	O11727	O11727 measles vir
145	4	100.0	123	16	Q8XBL2	Q8xb12 escherichia	218	4	100.0	161	12	O11728	O11728 measles vir
146	4	100.0	124	11	Q9DIL5	Q9dil5 mus musculu	219	4	100.0	161	12	O11729	O11729 measles vir
147	4	100.0	124	16	O53161	O53161 mycobacteri	220	4	100.0	161	12	O11730	O11730 measles vir
148	4	100.0	126	17	O30093	O30093 archaeoglob	221	4	100.0	161	12	O11731	O11731 measles vir
149	4	100.0	127	16	Q8RF32	Q8rf32 fusobacteri	222	4	100.0	161	12	O11732	O11732 measles vir
150	4	100.0	127	17	Q9HIN3	Q9hin3 thermoplas	223	4	100.0	161	12	O11733	O11733 measles vir
151	4	100.0	127	17	Q97BY4	Q97by4 thermoplas	224	4	100.0	161	12	O11734	O11734 measles vir
152	4	100.0	127	17	Q8TM59	Q8tm59 methanosarc	225	4	100.0	161	12	O11735	O11735 measles vir
153	4	100.0	128	8	P92858	P92858 monotonus	226	4	100.0	161	12	O11736	O11736 measles vir
154	4	100.0	128	9	Q9AZJ7	Q9azj7 bacterioph	227	4	100.0	161	17	O11737	O11737 measles vir
155	4	100.0	128	16	Q9CJF6	Q9cjf6 lactococcus	228	4	100.0	161	17	Q8ZUL6	Q8zul6 pyrobaculum
156	4	100.0	128	16	Q8YFV6	Q8yfv6 brucella me	229	4	100.0	162	10	Q8S0K1	Q8s0k1 oryza sativ
157	4	100.0	132	5	Q9V7T4	Q9v7t4 drosophila	230	4	100.0	164	10	Q8S450	Q8s450 mencha long
158	4	100.0	133	2	Q9FAY8	Q9fay8 streptococc	231	4	100.0	165	16	Q97HN9	Q97hn9 clostridium
159	4	100.0	133	16	Q92PQ6	Q92pq6 rhizobium m	232	4	100.0	165	16	Q98PL4	Q98pl4 mycoplasma
160	4	100.0	134	5	Q9V6B2	Q9v6b2 drosophila	233	4	100.0	166	16	Q9A356	Q9a356 caulobacter
161	4	100.0	134	12	Q9YZB5	Q9yzb5 human calic	234	4	100.0	166	17	Q8TKW8	Q8tkw8 methanosarc
162	4	100.0	135	9	Q8SC48	Q8sc48 strx2 conver	235	4	100.0	167	4	O60844	O60844 homo sapien



236	4	100.0	168	2	Q9RB47	Q9rb47 clostridium	309	4	100.0	189	16	Q828U2	Q828u2 salmonella
237	4	100.0	168	4	Q96DD9	Q96dd9 homo sapien	310	4	100.0	190	2	Q9S0I8	Q9s0i8 borrelia bu
238	4	100.0	168	10	Q9LIX2	Q9lix2 glycine max	311	4	100.0	190	2	Q9S099	Q9s099 borrelia bu
239	4	100.0	168	12	Q8OL19	Q8qli9 mamestra co	312	4	100.0	190	16	Q8XJF7	Q8xjf7 clostridium
240	4	100.0	168	17	Q8ZWK1	Q8zwk1 pyrobaculum	313	4	100.0	190	16	Q8XDX3	Q8xdx3 escherichia
241	4	100.0	169	2	P70923	P70923 bacillus il	314	4	100.0	191	2	Q9S401	Q9s401 proteus mir
242	4	100.0	169	4	Q8TAU4	Q8tau4 homo sapien	315	4	100.0	191	2	Q9X735	Q9x735 escherichia
243	4	100.0	169	11	Q8RS97	Q8rs97 mus musculu	316	4	100.0	191	16	Q9LAN9	Q9lan9 escherichia
244	4	100.0	169	16	Q8X9D6	Q8xd6 escherichia	317	4	100.0	192	5	Q9VPD0	Q9vpd0 drosophila
245	4	100.0	169	16	Q9Z988	Q9z988 chlamydia p	318	4	100.0	192	16	Q8XLS1	Q8xls1 clostridium
246	4	100.0	170	8	Q9S8M2	Q9s8m2 rhododendro	319	4	100.0	193	2	Q30699	Q30699 acetobacter
247	4	100.0	170	16	Q50996	Q50996 borrelia bu	320	4	100.0	194	2	Q9ADT6	Q9adt6 salmonella
248	4	100.0	170	16	Q9PNT8	Q9pnt8 campylobact	321	4	100.0	194	10	Q9LEW1	Q9lew1 arabidopsis
249	4	100.0	171	2	Q9X553	Q9x553 salmonella	322	4	100.0	194	12	Q04393	Q04393 acholeplasm
250	4	100.0	171	16	Q9PMV6	Q9pmv6 campylobact	323	4	100.0	194	16	Q8RHK1	Q8rhk1 fusobacteri
251	4	100.0	171	16	Q9A3Z0	Q9a3z0 caulobacter	324	4	100.0	195	2	Q93AV4	Q93av4 serratia ma
252	4	100.0	171	17	Q97Z09	Q97z09 sulfolobus	325	4	100.0	195	3	Q93948	Q93948 canidia alb
253	4	100.0	172	5	O15628	O15628 entamoeba h	326	4	100.0	195	12	Q66056	Q66056 canine herp
254	4	100.0	172	8	Q9S8M1	Q9s8m1 ledum groen	327	4	100.0	195	12	Q9J836	Q9j836 spodoptera
255	4	100.0	173	5	Q8SRT5	Q8srt5 encephalito	328	4	100.0	196	5	Q9SVZ8	Q9svz8 drosophila
256	4	100.0	173	8	Q9S8N5	Q9sbns pyrolo aphy	329	4	100.0	197	5	Q9SM07	Q9sm07 drosophila
257	4	100.0	173	8	Q9S8N4	Q9sbm5 pyrolo pict	330	4	100.0	197	5	Q9SM06	Q9sm06 drosophila
258	4	100.0	173	8	Q9S8N2	Q9sbm2 arctostaphy	331	4	100.0	197	5	Q9SM04	Q9sm04 drosophila
259	4	100.0	173	8	Q9S8N1	Q9sbm1 arctostaphy	332	4	100.0	197	5	Q9SM03	Q9sm03 drosophila
260	4	100.0	173	8	Q9S8M0	Q9sbm0 enkiantbus	333	4	100.0	197	5	Q9SM02	Q9sm02 drosophila
261	4	100.0	173	10	Q9XGSS	Q9xgs5 oryza sativ	334	4	100.0	197	5	Q9SVZ9	Q9svz9 drosophila
262	4	100.0	173	10	Q9XGSA	Q9xgs4 oryza sativ	335	4	100.0	197	5	Q8SVP7	Q8svp7 encephalito
263	4	100.0	173	10	Q9FU46	Q9fua6 lolium pere	336	4	100.0	198	11	Q9COC9	Q9coc9 mus musculu
264	4	100.0	173	16	Q9K215	Q9k215 chlamydia p	337	4	100.0	198	11	Q99JZ4	Q99jz4 mus musculu
265	4	100.0	174	2	Q56862	Q56862 yerinia en	338	4	100.0	198	11	Q9QVY3	Q9qv3 cricetus
266	4	100.0	174	8	Q9S8M0	Q9sbm0 comarostaph	339	4	100.0	198	11	Q9QVY2	Q9qv2 cricetus
267	4	100.0	174	8	Q9S8M9	Q9sbm0 gaultheria	340	4	100.0	198	11	Q9QVY2	Q9qv2 cricetus
268	4	100.0	174	8	Q9S8M7	Q9sbm7 vaccinium s	341	4	100.0	199	5	O76321	O76321 streptococc
269	4	100.0	174	8	Q9S8M5	Q9sbm5 leucothoe a	342	4	100.0	199	5	O45369	O45369 caenorhabdi
270	4	100.0	174	8	Q9S8M4	Q9sbm4 pieris phil	343	4	100.0	199	5	Q9SM00	Q9sm00 drosophila
271	4	100.0	174	8	Q9S8M3	Q9sbm3 oxydendrum	344	4	100.0	200	2	P97174	P97174 mycobacteri
272	4	100.0	174	8	Q9S8L9	Q9sb19 enkiantbus	345	4	100.0	200	4	Q8TBF0	Q8tbf0 homo sapien
273	4	100.0	174	16	Q8Y1Q2	Q8y1q2 ralstonia s	346	4	100.0	200	5	Q9SM05	Q9sm05 drosophila
274	4	100.0	175	2	Q9RI16	Q9ri16 salmonella	347	4	100.0	200	5	Q9SM01	Q9sm01 drosophila
275	4	100.0	175	4	Q9P128	Q9p128 homo sapien	348	4	100.0	200	5	Q9SVZ7	Q9svz7 drosophila
276	4	100.0	175	10	Q9S6C6	Q9s6c6 arabidopsis	349	4	100.0	201	11	Q9EQN0	Q9eqn0 mus musculu
277	4	100.0	175	12	Q9Q5K4	Q9q5k4 avian infec	350	4	100.0	201	16	Q97J72	Q97j72 clostridium
278	4	100.0	176	4	Q9H9M8	Q9h9m8 homo sapien	351	4	100.0	202	11	Q63304	Q63304 rattus norv
279	4	100.0	176	5	Q20750	Q20750 caenorhabdi	352	4	100.0	202	11	Q9S0G4	Q9s0g4 borrelia bu
280	4	100.0	176	10	Q9M500	Q9m5g0 oryza sativ	353	4	100.0	203	2	Q9S0D2	Q9s0d2 borrelia bu
281	4	100.0	176	17	Q9UXL8	Q9uxl8 sulfolobus	354	4	100.0	203	2	Q9S0D6	Q9s0d6 borrelia bu
282	4	100.0	176	17	Q9UXL8	Q9uxl8 sulfolobus	355	4	100.0	203	2	Q9S0D6	Q9s0d6 borrelia bu
283	4	100.0	179	3	Q07951	Q07951 saccharomyc	356	4	100.0	203	2	O52985	O52985 escherichia
284	4	100.0	180	2	Q9X9T2	Q9x9t2 synchococc	357	4	100.0	203	5	P90944	P90944 caenorhabdi
285	4	100.0	180	10	Q93VE6	Q93ve6 arabidopsis	358	4	100.0	203	10	O65038	O65038 oryza sativ
286	4	100.0	181	11	Q9D7M1	Q9d7m1 mus musculu	359	4	100.0	204	2	O56450	O56450 xanthomonas
287	4	100.0	181	11	Q9D7R3	Q9d7r3 mus musculu	360	4	100.0	204	2	O66023	O66023 pseudomonas
288	4	100.0	181	16	Q9S266	Q9s266 streptomyc	361	4	100.0	204	2	Q9F3W2	Q9f3w2 pseudomonas
289	4	100.0	182	3	Q94583	Q94583 schizosacch	362	4	100.0	204	2	Q937A4	Q937a4 pseudomonas
290	4	100.0	182	10	Q9LJD7	Q9ljd7 arabidopsis	363	4	100.0	204	2	Q9JLM8	Q9jlm8 rhizobium m
291	4	100.0	182	16	Q9RZB1	Q9rzb1 deinococcus	364	4	100.0	204	10	Q9LFC8	Q9lfc8 arabidopsis
292	4	100.0	183	8	Q94KJ1	Q94kz1 schizopyll	365	4	100.0	204	10	Q94I88	Q94i88 atropa bell
293	4	100.0	183	12	O73552	O73552 spodoptera	366	4	100.0	204	17	Q8U3W9	Q8u3w9 pyrococcus
294	4	100.0	183	16	P74481	P74481 synchocyst	367	4	100.0	205	5	Q22782	Q22782 caenorhabdi
295	4	100.0	183	17	Q973R3	Q973r3 sulfolobus	368	4	100.0	206	10	Q9LV79	Q9lv79 arabidopsis
296	4	100.0	184	10	Q94FW9	Q94fw9 sorghum bic	369	4	100.0	207	10	Q9XIS8	Q9x1s8 glycine max
297	4	100.0	184	17	Q8ZNV7	Q8zxn7 pyrobaculum	370	4	100.0	207	2	Q48385	Q48385 klebsiella
298	4	100.0	185	2	O52945	O52945 bacillus su	371	4	100.0	207	3	Q9P7A1	Q9p7a1 schizosacch
299	4	100.0	186	10	Q9ZRH0	Q9zrh0 oryza sativ	372	4	100.0	207	5	Q9W692	Q9w692 plasmodium
300	4	100.0	186	10	Q9XHT6	Q9xht6 arabidopsis	373	4	100.0	207	5	Q26000	Q26000 plasmodium
301	4	100.0	187	5	Q8SWA7	Q8swa7 encephalito	374	4	100.0	207	10	Q9SID8	Q9sid8 arabidopsis
302	4	100.0	187	10	Q8W0U6	Q8w0u6 sorghum bic	375	4	100.0	207	10	Q9LFT9	Q9lft9 arabidopsis
303	4	100.0	187	17	O58979	O58979 pyrococcus	376	4	100.0	207	10	O8M3K5	O8m3k5 matricaria
304	4	100.0	187	17	Q974H5	Q974h5 sulfolobus	377	4	100.0	208	4	Q9UBE4	Q9ube4 homo sapien
305	4	100.0	188	5	Q9BKPO	Q9bkp0 caenorhabdi	378	4	100.0	208	5	O16280	O16280 caenorhabdi
306	4	100.0	189	2	O24764	O24764 hypnomicrob	379	4	100.0	208	5	O18334	O18334 drosophila
307	4	100.0	189	5	Q19169	Q19169 caenorhabdi	380	4	100.0	208	10	O80501	O80501 arabidopsis
308	4	100.0	189	16	Q8ZRB1	Q8zrb1 salmoneella	381	4	100.0	208	10	Q40525	Q40525 nitoclitana t

382	4	100.0	208	10	Q39869	Q39869 glycine max	455	4	100.0	222	11	Q61073	Q61073 mus musculus
383	4	100.0	208	11	Q8VEES	Q8vees mus musculus	456	4	100.0	223	16	Q984H8	Q984h8 rhizobium l
384	4	100.0	208	16	Q8YDES	Q8ydes bruceella me	457	4	100.0	223	16	Q8RDM7	Q8rdm7 fusbacteri
385	4	100.0	209	2	Q9LAE1	Q9lae1 streptococc	458	4	100.0	224	5	Q20115	Q20115 caenorhabdi
386	4	100.0	209	2	Q9LAE0	Q9lae0 streptococc	459	4	100.0	224	10	Q9LTS9	Q9lts9 arabidopsis
387	4	100.0	209	2	Q9LAD9	Q9lad9 streptococc	460	4	100.0	224	12	Q9Q889	Q9qb89 yaba monkey
388	4	100.0	209	2	Q9LAD8	Q9lad8 streptococc	461	4	100.0	224	12	Q9Q8Y8	Q9q8y8 shope fibro
389	4	100.0	209	2	Q9LAD7	Q9lad7 streptococc	462	4	100.0	224	12	Q9Q8L0	Q9q8l0 myxoma viru
390	4	100.0	209	2	Q9LAD5	Q9lad5 streptococc	463	4	100.0	224	12	Q9Q8H1	Q9q8h1 yaba-like d
391	4	100.0	209	2	Q9LAD4	Q9lad4 streptococc	464	4	100.0	224	12	Q8V4X4	Q8v4x4 monkeypox v
392	4	100.0	209	2	Q9LAD3	Q9lad3 streptococc	465	4	100.0	224	12	Q8V3K7	Q8v3k7 swinepox vi
393	4	100.0	209	2	Q9LAD2	Q9lad2 streptococc	466	4	100.0	224	12	Q8V2Q4	Q8v2q4 camelpox vi
394	4	100.0	209	2	Q9LAD1	Q9lad1 streptococc	467	4	100.0	224	12	Q8QM08	Q8qmu8 cowpox viru
395	4	100.0	209	2	Q9LAD0	Q9lad0 streptococc	468	4	100.0	224	16	Q25220	Q25220 helicobacte
396	4	100.0	209	2	Q9LAC9	Q9lac9 streptococc	469	4	100.0	224	16	Q9ZLZ9	Q9zlt9 helicobacte
397	4	100.0	209	2	Q9LAC8	Q9lac8 streptococc	470	4	100.0	225	2	Q9RPT3	Q9rpt3 uncultured
398	4	100.0	209	2	Q9LAC7	Q9lac7 streptococc	471	4	100.0	225	4	Q96KY7	Q96ky7 homo sapien
399	4	100.0	209	2	Q9LAC5	Q9lac5 streptococc	472	4	100.0	225	12	Q9WLK5	Q9wik5 hepatitis e
400	4	100.0	209	2	Q9LAC4	Q9lac4 streptococc	473	4	100.0	225	12	Q9QQT0	Q9qqt0 avian infec
401	4	100.0	209	2	Q9LAC3	Q9lac3 streptococc	474	4	100.0	226	2	Q9ZB14	Q9zbl4 leuconostoc
402	4	100.0	209	2	Q93KR1	Q93krl yersinia en	475	4	100.0	227	4	Q13445	Q13445 homo sapien
403	4	100.0	209	5	Q9NHB1	Q9nhb1 toxoplasma	476	4	100.0	227	10	Q9LTS8	Q9lts8 arabidopsis
404	4	100.0	209	16	Q9A627	Q9a627 caulobacter	477	4	100.0	227	12	Q9LRU0	Q9lru0 lumpy skin
405	4	100.0	209	16	Q98GV3	Q98gv3 rhizobium l	478	4	100.0	227	16	Q97MJ8	Q97mj8 clostridium
406	4	100.0	209	16	Q97PK8	Q97pk8 streptococc	479	4	100.0	228	2	Q9RDU2	Q9rdu2 pseudomonas
407	4	100.0	209	16	Q8UJ06	Q8uj06 agrobacteri	480	4	100.0	228	10	Q9FG88	Q9fg88 arabidopsis
408	4	100.0	209	16	Q92T49	Q92t49 rhizobium m	481	4	100.0	228	12	Q98271	Q98271 molluscum c
409	4	100.0	210	10	Q9MI35	Q9mi35 arabidopsis	482	4	100.0	229	10	Q8VY56	Q8vy56 arabidopsis
410	4	100.0	210	16	Q9A3P3	Q9a3p3 caulobacter	483	4	100.0	229	12	Q96587	Q96587 avian adeno
411	4	100.0	211	5	Q25707	Q25707 plasmodium	484	4	100.0	229	16	Q8XIV8	Q8xiv8 clostridium
412	4	100.0	212	10	Q9SLC0	Q9slc0 arabidopsis	485	4	100.0	229	17	Q9TRV4	Q9trv4 methanosarc
413	4	100.0	212	16	Q98DB5	Q98db5 rhizobium l	486	4	100.0	230	2	Q9X9S2	Q9x9s2 streptococc
414	4	100.0	213	5	Q9TY76	Q9ty76 plasmodium	487	4	100.0	230	2	Q8VVB5	Q8vvb5 streptococc
415	4	100.0	213	5	Q9TY75	Q9ty75 plasmodium	488	4	100.0	230	16	Q97PG5	Q97pg5 streptococc
416	4	100.0	213	5	Q9TY73	Q9ty73 plasmodium	489	4	100.0	231	10	Q9SV79	Q9sv79 arabidopsis
417	4	100.0	213	5	Q9TY72	Q9ty72 plasmodium	490	4	100.0	231	16	Q99Z29	Q99z29 streptococc
418	4	100.0	213	5	Q25928	Q25928 plasmodium	491	4	100.0	232	12	Q91MS1	Q91ms1 lumpy skin
419	4	100.0	213	5	Q9TY70	Q9ty70 plasmodium	492	4	100.0	232	17	Q58291	Q58291 pyrococcus
420	4	100.0	213	5	Q25939	Q25939 plasmodium	493	4	100.0	232	17	Q9UYL9	Q9uy19 pyrococcus
421	4	100.0	214	5	Q25926	Q25926 plasmodium	494	4	100.0	233	10	Q9SV73	Q9sv73 arabidopsis
422	4	100.0	214	5	Q25927	Q25927 plasmodium	495	4	100.0	233	16	Q9CIMO	Q9cim0 lactococcus
423	4	100.0	214	5	Q25930	Q25930 plasmodium	496	4	100.0	233	16	Q99XW1	Q99xw1 streptococc
424	4	100.0	214	5	Q25931	Q25931 plasmodium	497	4	100.0	233	16	Q9Z9N7	Q9z9n7 listeria in
425	4	100.0	214	5	Q25934	Q25934 plasmodium	498	4	100.0	234	11	Q9D224	Q9dbj7 salmonella
426	4	100.0	214	5	Q25936	Q25936 plasmodium	499	4	100.0	236	2	Q93BJ7	Q93bj7 salmonella
427	4	100.0	214	5	Q25937	Q25937 plasmodium	500	4	100.0	236	8	Q9WMT2	Q9wmt2 oenothera h
428	4	100.0	214	5	Q25938	Q25938 plasmodium	501	4	100.0	236	8	Q9BAS6	Q9bbe6 lotus japon
429	4	100.0	214	5	Q25943	Q25943 plasmodium	502	4	100.0	236	10	Q886G1	Q886g1 oryza sativ
430	4	100.0	214	10	Q9LY22	Q9ly22 arabidopsis	503	4	100.0	236	13	P79899	P79899 oncorhynch
431	4	100.0	214	10	Q9SMR4	Q9smr4 arabidopsis	504	4	100.0	236	13	P79905	P79905 salmo salar
432	4	100.0	215	5	Q25935	Q25935 plasmodium	505	4	100.0	237	2	Q93BW2	Q93bw2 salmonella
433	4	100.0	215	5	Q25940	Q25940 plasmodium	506	4	100.0	239	2	Q93BX3	Q93bx3 salmonella
434	4	100.0	215	10	Q94TK5	Q94tk5 scherffellia	507	4	100.0	239	10	Q9SQ50	Q9sq50 abroma augu
435	4	100.0	215	10	Q8VMI1	Q8vmi1 arabidopsis	508	4	100.0	240	5	Q94663	Q94663 plasmodium
436	4	100.0	215	16	P72739	P72739 synecocyst	509	4	100.0	240	8	Q8WLM3	Q8wlm3 cistanche t
437	4	100.0	215	16	Q9WXZ9	Q9wxz9 thermotoga	510	4	100.0	240	8	Q8WLM2	Q8wlm2 cistanche t
438	4	100.0	215	17	Q8U0U2	Q8u0u2 pyrococcus	511	4	100.0	241	5	Q9U5S2	Q9u5s2 entodinium
439	4	100.0	216	3	Q9P7W9	Q9p7w9 schizosacch	512	4	100.0	243	11	Q9UJRA	Q9ujra mus musculus
440	4	100.0	216	10	Q9LD16	Q9ld16 glycine max	513	4	100.0	243	16	Q8UK87	Q8uk87 agrobacteri
441	4	100.0	216	10	Q9ATV1	Q9atv1 glycine max	514	4	100.0	243	16	Q8U504	Q8u504 agrobacteri
442	4	100.0	216	16	Q9CNL1	Q9cnl1 pasteurella	515	4	100.0	244	5	Q9SRT3	Q9srt3 drosophila
443	4	100.0	216	16	Q92B15	Q92b15 listeria in	516	4	100.0	244	5	Q9VCB9	Q9vcb9 drosophila
444	4	100.0	217	5	Q9VGJ8	Q9vgj8 arabidopsis	517	4	100.0	245	8	Q8WLM7	Q8wlm7 cistanche d
445	4	100.0	217	10	Q9LJR8	Q9ljr8 arabidopsis	518	4	100.0	245	8	Q8WLM6	Q8wlm6 cistanche s
446	4	100.0	217	10	Q39898	Q39898 glycine max	519	4	100.0	245	8	Q8WLM5	Q8wlm5 cistanche s
447	4	100.0	217	10	Q39899	Q39899 glycine max	520	4	100.0	245	8	Q8WLM4	Q8wlm4 cistanche s
448	4	100.0	217	10	Q94IA1	Q94ia1 glycine max	521	4	100.0	245	12	Q81868	Q81868 hepatitis e
449	4	100.0	217	16	Q8UIB4	Q8uib4 agrobacteri	522	4	100.0	246	5	Q9UAV4	Q9uav4 caenorhabdi
450	4	100.0	217	16	Q92SFF6	Q92sf6 rhizobium m	523	4	100.0	247	2	Q93BX5	Q93bx5 salmonella
451	4	100.0	218	17	Q8TTI2	Q8tti2 methanosarc	524	4	100.0	248	2	Q9RFW9	Q9rfw9 mycoplasma
452	4	100.0	220	16	Q9A4I8	Q9a4i8 caulobacter	525	4	100.0	248	2	Q93MF0	Q93mf0 mycolatops
453	4	100.0	220	16	Q9A1H8	Q9a1h8 streptococc	526	4	100.0	248	5	O02399	O02399 teladorsagi
454	4	100.0	222	5	Q23188	Q23188 caenorhabdi	527	4	100.0	248	16	Q9A012	Q9a012 streptococc

528	4	100.0	248	17	Q97W42	Q97W42 sulfolobus	601	4	100.0	264	2	Q93BS5	Q93B65 salmonella
529	4	100.0	249	5	Q93BS1	Q93B61 salmonella	602	4	100.0	264	2	Q93BR7	Q93B77 salmonella
530	4	100.0	249	5	Q9W4U9	Q9W4U9 drosophila	603	4	100.0	264	2	Q93BQ6	Q93BQ6 salmonella
531	4	100.0	250	5	Q20262	Q20262 caenorhabdi	604	4	100.0	264	2	Q93BN9	Q93BN9 salmonella
532	4	100.0	250	6	Q95YCO	Q95YCO canis famli	605	4	100.0	264	2	Q93BM8	Q93BM8 salmonella
533	4	100.0	250	12	Q66069	Q66069 canine hezp	606	4	100.0	264	2	Q93BM7	Q93BM7 salmonella
534	4	100.0	251	2	Q93BP9	Q93BP9 salmonella	607	4	100.0	264	2	Q93BL6	Q93BL6 salmonella
535	4	100.0	251	11	Q9CWN6	Q9CWN6 mus musculus	608	4	100.0	264	2	Q93BK6	Q93BK6 salmonella
536	4	100.0	252	2	Q93BS9	Q93BS9 salmonella	609	4	100.0	264	2	Q93BJ4	Q93BJ4 salmonella
537	4	100.0	252	2	Q93BS8	Q93BS8 salmonella	610	4	100.0	264	2	Q93BI7	Q93BI7 salmonella
538	4	100.0	252	2	Q93BS6	Q93BS6 salmonella	611	4	100.0	264	2	Q93BI3	Q93BI3 salmonella
539	4	100.0	252	2	Q93BN3	Q93BN3 salmonella	612	4	100.0	264	2	Q93BH7	Q93BH7 salmonella
540	4	100.0	252	2	Q93BN2	Q93BN2 salmonella	613	4	100.0	264	2	Q93BH5	Q93BH5 salmonella
541	4	100.0	252	2	Q93BU9	Q93BU9 salmonella	614	4	100.0	264	2	Q93BH4	Q93BH4 salmonella
542	4	100.0	252	2	Q93BJ1	Q93BJ1 salmonella	615	4	100.0	264	2	Q934D0	Q934D0 salmonella
543	4	100.0	252	2	Q93JY1	Q93JY1 salmonella	616	4	100.0	264	2	Q934C9	Q934C9 salmonella
544	4	100.0	252	16	Q8X4L1	Q8X4L1 escherichia	617	4	100.0	264	2	Q934C8	Q934C8 salmonella
545	4	100.0	253	2	Q9KJ12	Q9KJ12 lactococcus	618	4	100.0	264	2	Q934A6	Q934A6 salmonella
546	4	100.0	253	2	Q93BN1	Q93BN1 salmonella	619	4	100.0	264	2	Q933X7	Q933X7 salmonella
547	4	100.0	253	2	Q93BK5	Q93BK5 salmonella	620	4	100.0	264	2	Q933T8	Q933T8 salmonella
548	4	100.0	253	16	Q93BK2	Q93BK2 salmonella	621	4	100.0	264	2	Q933T7	Q933T7 salmonella
549	4	100.0	253	16	Q8YMF2	Q8YMF2 anabaena sp	622	4	100.0	264	10	Q9MON9	Q9MON9 arabidopsis
550	4	100.0	253	16	Q8UKR7	Q8UKR7 agrobacteri	623	4	100.0	264	10	Q93619	Q93619 arabidopsis
551	4	100.0	253	16	Q8YCC1	Q8YCC1 bruceella me	624	4	100.0	265	2	Q93LK0	Q93LK0 escherichia
552	4	100.0	254	1	Q977T1	Q977T1 uncultured	625	4	100.0	265	2	Q93BY7	Q93BY7 salmonella
553	4	100.0	254	2	Q93BU5	Q93BU5 salmonella	626	4	100.0	265	2	Q93BY6	Q93BY6 salmonella
554	4	100.0	254	2	Q93BK8	Q93BK8 salmonella	627	4	100.0	265	2	Q93BY4	Q93BY4 salmonella
555	4	100.0	254	4	Q9HON0	Q9HON0 homo sapien	628	4	100.0	265	2	Q93BY3	Q93BY3 salmonella
556	4	100.0	254	10	Q82340	Q82340 arabidopsis	629	4	100.0	265	2	Q93BY2	Q93BY2 salmonella
557	4	100.0	255	2	Q46176	Q46176 chlamydomph	630	4	100.0	265	2	Q93BY0	Q93BY0 salmonella
558	4	100.0	256	2	Q93BU7	Q93BU7 salmonella	631	4	100.0	265	2	Q93BX7	Q93BX7 salmonella
559	4	100.0	256	5	Q8WQ07	Q8WQ07 osterltagia	632	4	100.0	265	2	Q93BX6	Q93BX6 salmonella
560	4	100.0	256	16	Q9RM13	Q9RM13 staphylococc	633	4	100.0	265	2	Q93BX4	Q93BX4 salmonella
561	4	100.0	257	2	Q93BU0	Q93BU0 salmonella	634	4	100.0	265	2	Q93BX2	Q93BX2 salmonella
562	4	100.0	258	2	Q93BZ0	Q93BZ0 salmonella	635	4	100.0	265	2	Q93BX1	Q93BX1 salmonella
563	4	100.0	258	2	Q93BR6	Q93BR6 salmonella	636	4	100.0	265	2	Q93BX0	Q93BX0 salmonella
564	4	100.0	258	2	Q93BM1	Q93BM1 salmonella	637	4	100.0	265	2	Q93BW9	Q93BW9 salmonella
565	4	100.0	258	10	Q49284	Q49284 arabidopsis	638	4	100.0	265	2	Q93BW6	Q93BW6 salmonella
566	4	100.0	258	16	Q8XINO	Q8XINO clostridium	639	4	100.0	265	2	Q93BM5	Q93BM5 salmonella
567	4	100.0	259	2	Q93BV2	Q93BV2 salmonella	640	4	100.0	265	2	Q93BM1	Q93BM1 salmonella
568	4	100.0	259	16	Q9KB14	Q9KB14 bacillus ha	641	4	100.0	265	2	Q93BM0	Q93BM0 salmonella
569	4	100.0	260	2	Q93BM4	Q93BM4 salmonella	642	4	100.0	265	2	Q93BV9	Q93BV9 salmonella
570	4	100.0	260	2	Q93BT6	Q93BT6 salmonella	643	4	100.0	265	2	Q93BV7	Q93BV7 salmonella
571	4	100.0	260	2	Q93BI6	Q93BI6 salmonella	644	4	100.0	265	2	Q93BV6	Q93BV6 salmonella
572	4	100.0	260	13	Q90YW4	Q90YW4 iccalurnus p	645	4	100.0	265	2	Q93BV5	Q93BV5 salmonella
573	4	100.0	260	16	Q9HYV6	Q9HYV6 pseudomonas	646	4	100.0	265	2	Q93BV3	Q93BV3 salmonella
574	4	100.0	261	2	Q93BU2	Q93BU2 salmonella	647	4	100.0	265	2	Q93BV1	Q93BV1 salmonella
575	4	100.0	261	2	Q93BT3	Q93BT3 salmonella	648	4	100.0	265	2	Q93BU6	Q93BU6 salmonella
576	4	100.0	261	2	Q93BS2	Q93BS2 salmonella	649	4	100.0	265	2	Q93BU1	Q93BU1 salmonella
577	4	100.0	261	2	Q93BR8	Q93BR8 salmonella	650	4	100.0	265	2	Q93BT9	Q93BT9 salmonella
578	4	100.0	261	2	Q93BR1	Q93BR1 salmonella	651	4	100.0	265	2	Q93BT8	Q93BT8 salmonella
579	4	100.0	261	2	Q93BM3	Q93BM3 salmonella	652	4	100.0	265	2	Q93BT5	Q93BT5 salmonella
580	4	100.0	261	2	Q93BL0	Q93BL0 salmonella	653	4	100.0	265	2	Q93BT2	Q93BT2 salmonella
581	4	100.0	261	2	Q93BK3	Q93BK3 salmonella	654	4	100.0	265	2	Q93BT1	Q93BT1 salmonella
582	4	100.0	261	2	Q93BI0	Q93BI0 salmonella	655	4	100.0	265	2	Q93BT0	Q93BT0 salmonella
583	4	100.0	261	2	Q93BH8	Q93BH8 salmonella	656	4	100.0	265	2	Q93BS7	Q93BS7 salmonella
584	4	100.0	261	10	Q9CZ24	Q9CZ24 populus tre	657	4	100.0	265	2	Q93BS4	Q93BS4 salmonella
585	4	100.0	261	16	Q9CFW3	Q9CFW3 lactococcus	658	4	100.0	265	2	Q93BS0	Q93BS0 salmonella
586	4	100.0	262	2	Q93BV8	Q93BV8 salmonella	659	4	100.0	265	2	Q93BR9	Q93BR9 salmonella
587	4	100.0	262	2	Q93BR4	Q93BR4 salmonella	660	4	100.0	265	2	Q93BR5	Q93BR5 salmonella
588	4	100.0	262	2	Q93BN5	Q93BN5 salmonella	661	4	100.0	265	2	Q93BR2	Q93BR2 salmonella
589	4	100.0	262	16	Q92D51	Q92D51 listeria in	662	4	100.0	265	2	Q93BR0	Q93BR0 salmonella
590	4	100.0	262	16	Q8Y8D5	Q8Y8D5 listeria mo	663	4	100.0	265	2	Q93BO9	Q93BO9 salmonella
591	4	100.0	263	2	Q93BM8	Q93BM8 salmonella	664	4	100.0	265	2	Q93BO7	Q93BO7 salmonella
592	4	100.0	263	2	Q93BIS	Q93BIS salmonella	665	4	100.0	265	2	Q93BO5	Q93BO5 salmonella
593	4	100.0	263	10	Q8S1M1	Q8S1M1 oryza sativ	666	4	100.0	265	2	Q93BQ4	Q93BQ4 salmonella
594	4	100.0	263	10	Q8QUM5	Q8QUM5 infectious	667	4	100.0	265	2	Q93BQ1	Q93BQ1 salmonella
595	4	100.0	263	16	Q8ZBF5	Q8ZBF5 yersinia pe	668	4	100.0	265	2	Q93BP8	Q93BP8 salmonella
596	4	100.0	264	2	Q93BM3	Q93BM3 salmonella	669	4	100.0	265	2	Q93BP7	Q93BP7 salmonella
597	4	100.0	264	2	Q93BV4	Q93BV4 salmonella	670	4	100.0	265	2	Q93BP6	Q93BP6 salmonella
598	4	100.0	264	2	Q93BU4	Q93BU4 salmonella	671	4	100.0	265	2	Q93BP5	Q93BP5 salmonella
599	4	100.0	264	2	Q93BT7	Q93BT7 salmonella	672	4	100.0	265	2	Q93BP4	Q93BP4 salmonella
600	4	100.0	264	2	Q93BT7	Q93BT7 salmonella	673	4	100.0	265	2	Q93BP4	Q93BP4 salmonella

674	4	100.0	265	2	Q93BP2	Q93bp2 salmonella	747	4	100.0	279	5	Q917C8	Q917c8 drosophila
675	4	100.0	265	2	Q93BP0	Q93bp0 salmonella	748	4	100.0	279	10	Q917C11	Q917c11 arabidopsis
676	4	100.0	265	2	Q93BN0	Q93bn0 salmonella	749	4	100.0	279	11	Q8CSN3	Q8csn3 mus musculus
677	4	100.0	265	2	Q93BM9	Q93bm9 salmonella	750	4	100.0	280	8	Q8SFF1	Q8sff1 phaeoprogne
678	4	100.0	265	2	Q93BM8	Q93bm8 salmonella	751	4	100.0	280	8	Q8SFF0	Q8sff0 progne subi
679	4	100.0	265	2	Q93BM6	Q93bm6 salmonella	752	4	100.0	280	8	Q8SFE8	Q8sfe8 tachycineta
680	4	100.0	265	2	Q93BM5	Q93bm5 salmonella	753	4	100.0	280	8	Q8SFE7	Q8sfe7 tachycineta
681	4	100.0	265	2	Q93BM4	Q93bm4 salmonella	754	4	100.0	280	8	Q8SFE6	Q8sfe6 tachycineta
682	4	100.0	265	2	Q93BM2	Q93bm2 salmonella	755	4	100.0	280	8	Q8SFE5	Q8sfe5 tachycineta
683	4	100.0	265	2	Q93BM0	Q93bm0 salmonella	756	4	100.0	280	8	Q8SFE4	Q8sfe4 tachycineta
684	4	100.0	265	2	Q93BL9	Q93bl9 salmonella	757	4	100.0	280	8	Q8SFE3	Q8sfe3 tachycineta
685	4	100.0	265	2	Q93BL8	Q93bl8 salmonella	758	4	100.0	280	8	Q8SFE2	Q8sfe2 tachycineta
686	4	100.0	265	2	Q93BL7	Q93bl7 salmonella	759	4	100.0	280	8	Q8SFE1	Q8sfe1 tachycineta
687	4	100.0	265	2	Q93BL4	Q93bl4 salmonella	760	4	100.0	280	16	Q97GY9	Q97gy9 clostridium
688	4	100.0	265	2	Q93BL3	Q93bl3 salmonella	761	4	100.0	280	16	Q95WM6	Q95wm6 staphylococ
689	4	100.0	265	2	Q93BL2	Q93bl2 salmonella	762	4	100.0	281	5	O44774	O44774 caenorhabdi
690	4	100.0	265	2	Q93BL1	Q93bl1 salmonella	763	4	100.0	281	17	Q8ZT96	Q8zt96 pyrobaculum
691	4	100.0	265	2	Q93BK7	Q93bk7 salmonella	764	4	100.0	282	12	Q91B96	Q91b96 spodoptera
692	4	100.0	265	2	Q93BK4	Q93bk4 salmonella	765	4	100.0	282	16	Q92DJ8	Q92dj8 listeria in
693	4	100.0	265	2	Q93BK1	Q93bk1 salmonella	766	4	100.0	282	16	Q8Y8S5	Q8y8s5 listeria mo
694	4	100.0	265	2	Q93BJ8	Q93bj8 salmonella	767	4	100.0	282	16	Q8Y8S3	Q8y8s3 mycoplasma
695	4	100.0	265	2	Q93BJ5	Q93bj5 salmonella	768	4	100.0	282	16	Q8YPK5	Q8ypk5 anabaena sp
696	4	100.0	265	2	Q93BJ3	Q93bj3 salmonella	769	4	100.0	283	10	Q9LQC0	Q9lqc0 arabidopsis
697	4	100.0	265	2	Q93BJ2	Q93bj2 salmonella	770	4	100.0	283	10	Q94FX2	Q94fx2 arabidopsis
698	4	100.0	265	2	Q93BI9	Q93bi9 salmonella	771	4	100.0	283	16	Q916R2	Q916r2 pseudomonas
699	4	100.0	265	2	Q93BI8	Q93bi8 salmonella	772	4	100.0	284	5	Q18863	Q18863 caenorhabdi
700	4	100.0	265	2	Q93BI4	Q93bi4 salmonella	773	4	100.0	285	5	P91556	P91556 caenorhabdi
701	4	100.0	265	2	Q93BI1	Q93bi1 salmonella	774	4	100.0	285	16	Q8UGJ5	Q8ugj5 agrobacteri
702	4	100.0	265	2	Q934B8	Q934b8 salmonella	775	4	100.0	286	4	Q96JZ4	Q96jz4 homo sapien
703	4	100.0	265	2	Q933Z7	Q933z7 salmonella	776	4	100.0	286	11	Q921E3	Q921e3 mus musculus
704	4	100.0	265	2	Q933X0	Q933x0 salmonella	777	4	100.0	287	12	Q9DVV3	Q9dvv3 pluteella xy
705	4	100.0	265	2	Q933W9	Q933w9 salmonella	778	4	100.0	287	16	Q92EY6	Q92ey6 listeria in
706	4	100.0	265	2	Q933V9	Q933v9 salmonella	779	4	100.0	287	16	Q8YA65	Q8ya65 listeria mo
707	4	100.0	265	2	Q933J4	Q933j4 salmonella	780	4	100.0	287	17	Q8U3L6	Q8u3l6 pyrococcus
708	4	100.0	265	2	Q933I9	Q933i9 salmonella	781	4	100.0	288	4	Q8WM97	Q8wm97 homo sapien
709	4	100.0	265	2	Q933H8	Q933h8 salmonella	782	4	100.0	288	4	Q8TBK5	Q8tbk5 homo sapien
710	4	100.0	265	2	Q933H0	Q933h0 salmonella	783	4	100.0	288	5	Q9V614	Q9v614 drosophila
711	4	100.0	265	2	Q933G3	Q933g3 salmonella	784	4	100.0	288	17	Q97914	Q97914 thermoplasma
712	4	100.0	265	2	Q933E9	Q933e9 salmonella	785	4	100.0	289	4	Q9HBB3	Q9hbb3 homo sapien
713	4	100.0	265	2	Q933D6	Q933d6 salmonella	786	4	100.0	289	16	Q928T0	Q928t0 chlamydia p
714	4	100.0	265	2	Q932T1	Q932t1 salmonella	787	4	100.0	289	16	Q8XTP2	Q8xtp2 ralstonia s
715	4	100.0	265	2	Q932S9	Q932s9 salmonella	788	4	100.0	289	17	Q97A01	Q97a01 thermoplasma
716	4	100.0	265	2	Q932R1	Q932r1 salmonella	789	4	100.0	290	11	Q9CTA3	Q9cta3 mus musculus
717	4	100.0	265	2	Q932Q1	Q932q1 salmonella	790	4	100.0	290	16	Q928Z0	Q928z0 listeria in
718	4	100.0	265	5	Q9N5Z7	Q9n5z7 caenorhabdi	791	4	100.0	291	4	Q96GZ1	Q96gz1 homo sapien
719	4	100.0	265	16	Q9X1T2	Q9x1t2 thermotoga	792	4	100.0	291	5	Q9NJV2	Q9njv2 haemophilus
720	4	100.0	266	17	O59281	O59281 pyrococcus	793	4	100.0	291	11	O35746	O35746 spallax leuc
721	4	100.0	266	17	Q9V137	Q9v137 pyrococcus	794	4	100.0	291	11	O8VHZ7	O8vhz7 mus musculus
722	4	100.0	266	17	O8U0K6	O8u0k6 pyrococcus	795	4	100.0	291	11	Q9CYT5	Q9cyt5 mus musculus
723	4	100.0	267	16	Q91OG0	Q91og0 pseudomonas	796	4	100.0	291	16	Q9PHR6	Q9phr6 campylobact
724	4	100.0	268	10	Q9FM16	Q9fm16 arabidopsis	797	4	100.0	292	4	Q9H7W3	Q9h7w3 homo sapien
725	4	100.0	268	11	O8VBZ6	O8vbz6 mus musculus	798	4	100.0	292	10	O81075	O81075 arabidopsis
726	4	100.0	268	17	Q9YFH2	Q9yfh2 aeropyrum p	799	4	100.0	292	13	Q9YGM4	Q9ygm4 gallus gall
727	4	100.0	269	3	O94440	O94440 schizosacch	800	4	100.0	292	17	Q9YR99	Q9yr99 aeropyrum p
728	4	100.0	269	5	Q8SPS5	Q8sps5 dictyosteli	801	4	100.0	293	5	O8SSA1	O8ssal encephalito
729	4	100.0	269	16	Q97RA2	Q97ra2 streptococc	802	4	100.0	294	16	Q9FUF9	Q9fuf9 campylobact
730	4	100.0	270	16	Q9Z872	Q9z872 chlamydia p	803	4	100.0	294	16	Q97NL9	Q97nl9 streptococc
731	4	100.0	270	16	O8RTA1	O8rel4 fusobacteri	804	4	100.0	295	2	P95534	P95534 pseudomonas
732	4	100.0	270	17	O8TKA1	O8tkal methanosarc	805	4	100.0	295	5	O9UZE7	O9uze7 caenorhabdi
733	4	100.0	271	10	Q9SXX4	Q9sxx4 arabidopsis	806	4	100.0	295	5	O9N3X7	O9n3x7 caenorhabdi
734	4	100.0	271	16	Q99T20	Q99tz0 staphylococ	807	4	100.0	295	11	Q9D6H0	Q9d6h0 mus musculus
735	4	100.0	272	5	Q9VEM1	Q9vem1 drosophila	808	4	100.0	295	16	Q9YNR8	Q9ynr8 anabaena sp
736	4	100.0	273	5	O9N3B9	Q9n3b9 caenorhabdi	809	4	100.0	296	8	Q958I3	Q958i3 hymenolepis
737	4	100.0	274	2	Q9RQL1	Q9rql1 borrelia va	810	4	100.0	296	11	Q925C3	Q925c3 mus musculus
738	4	100.0	274	2	O83037	O83037 borrelia va	811	4	100.0	297	2	Q9RFQ3	Q9rfq3 mycoplasma
739	4	100.0	274	2	Q9R423	Q9r423 borrelia bu	812	4	100.0	297	10	O8VY65	O8vy65 arabidopsis
740	4	100.0	274	16	O8ZS41	O8zs41 anabaena sp	813	4	100.0	297	16	Q910E6	Q910e6 pseudomonas
741	4	100.0	275	16	Q9K3N8	Q9k3n8 streptomyce	814	4	100.0	298	3	Q9Y847	Q9y847 kluyveromyc
742	4	100.0	276	2	O49502	O49502 mycoplasma	815	4	100.0	298	11	O8R254	O8r254 mus musculus
743	4	100.0	276	17	O8TWU2	O8twu2 methanopyru	816	4	100.0	298	13	O8UWG7	O8uwg7 gallus gall
744	4	100.0	277	5	O95QG7	O95qg7 caenorhabdi	817	4	100.0	298	16	Q97GR8	Q97gr8 clostridium
745	4	100.0	278	5	Q9GNP7	Q9gnp7 caenorhabdi	818	4	100.0	299	10	O48722	O48722 arabidopsis
746	4	100.0	279	2	Q9AET1	Q9aet1 aeromonas h	819	4	100.0	299	12	Q9EMK9	Q9emk9 amsacta moo

820	4	100.0	300	2	Q9WTC3	Q9WTC3 escherichia	893	4	100.0	314	11	Q9Z2H7	Q9Z2H7 mus musculus
821	4	100.0	300	3	Q74439	Q74439 schizosacch	894	4	100.0	314	16	Q8RTT4	Q8RTT4 fusobacteri
822	4	100.0	301	4	Q8TDU2	Q8TDU2 homo sapien	895	4	100.0	315	5	P91211	P91211 caenorhabdi
823	4	100.0	301	5	Q9Y201	Q9Y201 ephydactia f	896	4	100.0	315	10	Q9SVKO	Q9SVKO arabisdopsis
824	4	100.0	301	11	Q99KE7	Q99KE7 mus musculu	897	4	100.0	315	12	Q9DHN6	Q9DHN6 yaba-like d
825	4	100.0	302	16	Q8R878	Q8R878 thermoaer	898	4	100.0	315	16	Q9ZDX8	Q9ZDX8 rickettsia
826	4	100.0	302	2	Q9FI26	Q9FI26 bacillus ci	899	4	100.0	316	2	Q4B999	Q4B999 mycoplasma
827	4	100.0	303	5	Q45673	Q45673 caenorhabdi	900	4	100.0	316	4	Q9H111	Q9H111 homo sapien
828	4	100.0	303	10	Q9XHY0	Q9XHY0 cryza sativ	901	4	100.0	317	4	Q9EBJ2	Q9EBJ2 parametrix
829	4	100.0	303	16	Q9RC63	Q9RC63 bacillus ha	902	4	100.0	317	12	Q84614	Q84614 parametrix
830	4	100.0	304	3	Q8WZM8	Q8WZM8 neurospora	903	4	100.0	317	12	Q91KX4	Q91KX4 epinocia ap
831	4	100.0	304	5	Q25129	Q25129 halocynthia	904	4	100.0	318	5	Q8SRM6	Q8SRM6 encephalito
832	4	100.0	305	5	Q9TZC0	Q9TZC0 caenorhabdi	905	4	100.0	318	8	Q02684	Q02684 podospira a
833	4	100.0	306	16	Q9WZX0	Q9WZX0 thermotoga	906	4	100.0	319	5	Q9SP06	Q9SP06 tyranosoma
834	4	100.0	307	10	Q9FLV2	Q9FLV2 arabisdopsis	907	4	100.0	319	10	Q9SJVO	Q9SJVO arabisdopsis
835	4	100.0	307	5	Q9VKT6	Q9VKT6 drosophila	908	4	100.0	319	10	P82715	P82715 arabisdopsis
836	4	100.0	307	10	Q65548	Q65548 arabisdopsis	909	4	100.0	320	2	Q9RKU5	Q9RKU5 clostridium
837	4	100.0	307	11	Q8VBA5	Q8VBA5 mus musculu	910	4	100.0	320	5	Q21076	Q21076 caenorhabdi
838	4	100.0	308	5	Q23078	Q23078 caenorhabdi	911	4	100.0	320	13	Q8UVS3	Q8UVS3 xenopus lae
839	4	100.0	308	8	Q9MID5	Q9MID5 megacytiph	912	4	100.0	320	16	Q67816	Q67816 aquifex ae
840	4	100.0	308	10	Q65881	Q65881 populus tri	913	4	100.0	321	2	Q56873	Q56873 yersinia en
841	4	100.0	308	10	Q65882	Q65882 populus tri	914	4	100.0	321	5	Q9WCS2	Q9WCS2 drosophila
842	4	100.0	308	10	Q65904	Q65904 populus tri	915	4	100.0	321	10	Q49193	Q49193 striga asia
843	4	100.0	308	11	Q8R0L8	Q8R0L8 mus musculu	916	4	100.0	321	16	Q92AM3	Q92AM3 listeria in
844	4	100.0	309	4	Q8TBF3	Q8TBF3 homo sapien	917	4	100.0	321	16	Q8Y617	Q8Y617 listeria mo
845	4	100.0	309	5	Q16416	Q16416 caenorhabdi	918	4	100.0	322	2	Q9R9X8	Q9R9X8 pseudomonas
846	4	100.0	310	5	Q9UAW1	Q9UAW1 caenorhabdi	919	4	100.0	322	2	Q56868	Q56868 yersinia en
847	4	100.0	310	8	Q63624	Q63624 dalpulus ci	920	4	100.0	322	16	Q9WXT4	Q9WXT4 thermotoga
848	4	100.0	310	8	Q63626	Q63626 dalpulus el	921	4	100.0	323	2	Q87825	Q87825 staphylococ
849	4	100.0	310	8	Q63627	Q63627 dalpulus ge	922	4	100.0	323	16	Q9VFP1	Q9VFP1 staphylococ
850	4	100.0	310	8	Q63628	Q63628 dalpulus ge	923	4	100.0	324	17	Q97YC5	Q97YC5 sulfolobus
851	4	100.0	310	8	Q63629	Q63629 dalpulus gu	924	4	100.0	324	5	Q8SVH9	Q8SVH9 encephalito
852	4	100.0	310	8	Q63630	Q63630 dalpulus lo	925	4	100.0	324	16	Q92Y89	Q92Y89 ritzobium m
853	4	100.0	310	8	Q63631	Q63631 dalpulus ma	926	4	100.0	326	10	Q04214	Q04214 arabisdopsis
854	4	100.0	310	8	Q63632	Q63632 dalpulus ma	927	4	100.0	326	10	Q04714	Q04714 arabisdopsis
855	4	100.0	310	8	Q63633	Q63633 dalpulus ma	928	4	100.0	327	5	Q61923	Q61923 caenorhabdi
856	4	100.0	310	8	Q63634	Q63634 dalpulus qu	929	4	100.0	327	17	Q8Z2T0	Q8Z2T0 pyrobaculum
857	4	100.0	310	8	Q63637	Q63637 balclucha i	930	4	100.0	328	2	Q9F1X6	Q9F1X6 lactobacill
858	4	100.0	310	8	P92117	P92117 flexamia ar	931	4	100.0	328	2	Q85960	Q85960 sphingomona
859	4	100.0	310	8	P92115	P92115 flexamia ar	932	4	100.0	328	2	Q69253	Q69253 brucella me
860	4	100.0	310	8	P92095	P92095 flexamia ce	933	4	100.0	328	10	Q94FW8	Q94FW8 sorghum bic
861	4	100.0	310	8	P92113	P92113 flexamia ci	934	4	100.0	328	10	Q8RH22	Q8RH22 fusobacteri
862	4	100.0	310	8	P92089	P92089 flexamia da	935	4	100.0	329	5	Q9U2H7	Q9U2H7 caenorhabdi
863	4	100.0	310	8	P92088	P92088 flexamia de	936	4	100.0	329	10	Q43324	Q43324 populus can
864	4	100.0	310	8	P92090	P92090 flexamia do	937	4	100.0	329	10	Q9C975	Q9C975 arabisdopsis
865	4	100.0	310	8	P92091	P92091 flexamia fl	938	4	100.0	330	5	Q18189	Q18189 caenorhabdi
866	4	100.0	310	8	P92851	P92851 flexamia gr	939	4	100.0	330	12	Q9DSU0	Q9DSU0 ascovirus d
867	4	100.0	310	8	P92093	P92093 flexamia hu	940	4	100.0	330	16	Q9PR72	Q9PR72 ureaplasma
868	4	100.0	310	8	P92110	P92110 flexamia mo	941	4	100.0	330	16	Q9K6A6	Q9K6A6 bacillus ha
869	4	100.0	310	8	P92107	P92107 flexamia py	942	4	100.0	330	16	Q8ZFU9	Q8ZFU9 yersinia pe
870	4	100.0	310	8	P92080	P92080 flexamia se	943	4	100.0	330	17	Q8ZUJ2	Q8ZUJ2 pyrobaculum
871	4	100.0	310	8	P92106	P92106 flexamia st	944	4	100.0	331	2	Q9X7A3	Q9X7A3 mycobacteri
872	4	100.0	310	8	P92087	P92087 flexamia c	945	4	100.0	331	5	Q9XKN9	Q9XKN9 caenorhabdi
873	4	100.0	310	8	P92077	P92077 spartopyge	946	4	100.0	332	10	Q94CD9	Q94CD9 arabisdopsis
874	4	100.0	310	8	P92104	P92104 aflexia rub	947	4	100.0	332	16	Q9XK54	Q9XK54 vibrio chol
875	4	100.0	310	12	Q9QH52	Q9QH52 gallid herp	948	4	100.0	332	16	Q9X046	Q9X046 thermotoga
876	4	100.0	310	16	Q9V905	Q9V905 streptomyce	949	4	100.0	332	17	Q97WB9	Q97WB9 sulfolobus
877	4	100.0	311	2	Q9UPD8	Q9UPD8 neisseria m	950	4	100.0	333	5	Q9VSC2	Q9VSC2 drosophila
878	4	100.0	311	5	Q9NS12	Q9NS12 neisseria m	951	4	100.0	333	10	Q9FU76	Q9FU76 arabisdopsis
879	4	100.0	311	10	Q8W570	Q8W570 arabisdopsis	952	4	100.0	333	16	Q9CBH7	Q9CBH7 mycobacteri
880	4	100.0	311	11	Q8VF10	Q8VF10 mus musculu	953	4	100.0	333	17	Q8U115	Q8U115 pyrococcus
881	4	100.0	311	12	Q8DVR8	Q8DVR8 pluteia xy	954	4	100.0	334	2	Q9Z643	Q9Z643 enterobacte
882	4	100.0	311	16	Q9KOR4	Q9KOR4 neisseria m	955	4	100.0	334	5	Q8T8S1	Q8T8S1 drosophila
883	4	100.0	311	16	Q9JRB9	Q9JRB9 neisseria m	956	4	100.0	334	13	Q91974	Q91974 serinus can
884	4	100.0	311	16	Q8YJ18	Q8YJ18 ralsentonia s	957	4	100.0	335	2	Q54385	Q54385 brucella ab
885	4	100.0	312	8	Q94X50	Q94X50 dendropoma	958	4	100.0	335	10	Q9SCPO	Q9SCPO arabisdopsis
886	4	100.0	312	11	Q8VET0	Q8VET0 mus musculu	959	4	100.0	335	12	Q91BY6	Q91BY6 measles vir
887	4	100.0	313	10	Q98RP3	Q98RP3 guillardia	960	4	100.0	335	12	Q83716	Q83716 measles vir
888	4	100.0	313	12	Q41518	Q41518 grapevine l	961	4	100.0	335	12	Q83717	Q83717 measles vir
889	4	100.0	313	16	Q9KRX9	Q9KRX9 bacillus ha	962	4	100.0	335	12	Q83720	Q83720 measles vir
890	4	100.0	313	16	Q8RCA4	Q8RCA4 thermoaer	963	4	100.0	335	12	Q83721	Q83721 measles vir
891	4	100.0	314	5	Q76140	Q76140 trypanosoma	964	4	100.0	335	12	Q83723	Q83723 measles vir
892	4	100.0	314	5	Q76140	Q76140 trypanosoma	965	4	100.0	335	12	Q83723	Q83723 measles vir

966 4 100.0 335 12 Q83728 measles vir  
 967 4 100.0 335 12 Q83535 measles vir  
 968 4 100.0 335 12 Q83538 measles vir  
 969 4 100.0 335 12 Q86498 rinderpest  
 970 4 100.0 335 12 Q83624 measles vir  
 971 4 100.0 335 12 Q89120 measles vir  
 972 4 100.0 335 12 Q92055 measles vir  
 973 4 100.0 335 12 Q9WME6 measles vir  
 974 4 100.0 335 12 Q9QNM3 measles vir  
 975 4 100.0 335 12 Q9IFK5 measles vir  
 976 4 100.0 335 12 Q73507 peste-des-p  
 977 4 100.0 335 12 Q83529 measles vir  
 978 4 100.0 335 12 Q83712 measles vir  
 979 4 100.0 335 12 Q83718 measles vir  
 980 4 100.0 335 12 Q83722 measles vir  
 981 4 100.0 335 12 Q9IC34 measles vir  
 982 4 100.0 335 12 Q9IFK3 measles vir  
 983 4 100.0 335 12 Q93193 measles vir  
 984 4 100.0 335 12 Q04256 measles vir  
 985 4 100.0 335 12 Q9W850 measles vir  
 986 4 100.0 335 12 Q9W8A7 measles vir  
 987 4 100.0 335 12 Q04253 measles vir  
 988 4 100.0 335 12 Q04254 measles vir  
 989 4 100.0 335 12 Q09111 measles vir  
 990 4 100.0 335 13 Q9WQ06 gallus gall  
 991 4 100.0 335 16 Q8Z8P2 salmonella  
 992 4 100.0 335 16 Q8YH83 brucella me  
 993 4 100.0 336 2 Q00481 salmonella  
 994 4 100.0 336 5 Q25865 plasmodium  
 995 4 100.0 336 10 Q94155 oryza sativ  
 996 4 100.0 336 11 Q63775 rattus norv  
 997 4 100.0 336 12 Q66410 dolphin mor  
 998 4 100.0 336 16 Q98J14 rhizobium l  
 999 4 100.0 336 16 Q69510 mycobacteri  
 1000 4 100.0 338 2 Q9RMC0 acinetobact

## ALIGNMENTS

RESULT 1  
 Q9UH91 PRELIMINARY; PRT; 14 AA.

AC Q9UH91;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Xanthine oxidoreductase (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487118; PubMed=11034305;  
 RA Martelin E., Palvimo J.J., Lapatto R., Raivio K.O.;  
 RT "Nuclear factor Y activates the human xanthine oxidoreductase gene promoter";  
 RT FEBS Lett. 480:84-88(2000).  
 RL EMBL; AF203979; AAF15890.1; --  
 DR NON TER 14  
 SQ SEQUENCE 14 AA; 1626 MW; D300FB701792F0D2 CRC64;

Query Match 100.0%; Score 4; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 Db 5 KLVF 8

RESULT 2

Q9UCC8 PRELIMINARY; PRT; 19 AA.  
 AC Q9UCC8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Beta-amyloid-(1-42) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94068497; PubMed=8248178;  
 RA Rohrer A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,  
 RA Gowing E., Ball M.J.;  
 RT "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid  
 RT deposits; implications for the pathology of Alzheimer disease.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).  
 DR HSP; P05067; IAMB.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 SQ SEQUENCE 19 AA; 2315 MW; 05B02B3F6DDECE3E CRC64;

Query Match 100.0%; Score 4; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 Db 16 KLVF 19

RESULT 3

Q9UWG8 PRELIMINARY; PRT; 27 AA.  
 AC Q9UWG8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Keto-valine-ferredoxin oxidoreductase delta-subunit, VOR delta  
 DE (Fragment).  
 OS Thermococcus sp. (strain KI).  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Thermococcus.  
 OX NCBI\_TaxID=35749;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=ES-1;  
 RX MEDLINE=96146528; PubMed=8550513;  
 RA Heider J., Mai X., Adams M.W.;  
 RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a  
 RT new and reversible coenzyme A-dependent enzyme involved in peptide  
 RT fermentation by hyperthermophilic archaea.";  
 RL J. Bacteriol. 178:780-787(1996).  
 SQ SEQUENCE 27 AA; 3046 MW; 60C56F313C76E16C CRC64;

Query Match 100.0%; Score 4; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 Db 14 KLVF 17

RESULT 4

Q9UCD1 PRELIMINARY; PRT; 28 AA.  
 ID Q9UCD1  
 AC Q9UCD1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Beta-amyloid peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94045665; PubMed=8229004;  
RA Vigo-Pellfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;  
RT "Characterization of beta-amyloid peptide from human cerebrospinal  
RT fluid."  
RL J. Neurochem. 61:1965-1968 (1993).  
DR HSSP; P05067; 1AB4.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;  
  
Query Match 100.0%; Score 4; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVF 4  
DB 16 KLVF 19  
  
RESULT 5  
O9UC9 PRELIMINARY; PRT; 30 AA.  
ID O9UC9  
AC O9UC9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Beta-amyloid protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94153015; PubMed=8109908;  
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;  
RT "The amino acid sequence of neuritic plaque amyloid from a familial  
RT Alzheimer's disease patient."  
RL Ann. Neurol. 35:245-246 (1994).  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;  
  
Query Match 100.0%; Score 4; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVF 4  
DB 16 KLVF 19  
  
RESULT 6  
O9UC3 PRELIMINARY; PRT; 33 AA.  
ID O9UC3  
AC O9UC3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Beta-amyloid peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=93024877; PubMed=1406936;  
RA Seubert P., Vigo-Pellfrey C., Esch F., Dovey H., Davis D.,  
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;  
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from  
RT biological fluids."  
RL Nature 359:325-327 (1992).  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
SQ SEQUENCE 33 AA; 3674 MW; B1DEF2F4167ABD0 CRC64;  
  
Query Match 100.0%; Score 4; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVF 4  
DB 16 KLVF 19  
  
RESULT 7  
O52455 PRELIMINARY; PRT; 47 AA.  
ID O52455  
AC O52455;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last annotation update)  
DE Orf A (Fragment).  
OS Pyrococcus sp.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=33866;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IPREMER 585;  
RX MEDLINE=96144265; PubMed=8566767;  
RA Bouyoub A., Barbier G., Querellou J., Forterre P.;  
RT "A putative SOS repair gene (dinF-like) in a hyperthermophilic  
RT archaeon."  
RL Gene 167:147-149 (1995).  
DR EMBL; X91006; CAA62486.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 47 AA; 5541 MW; 828FC50C94800802 CRC64;  
  
Query Match 100.0%; Score 4; DB 1; Length 47;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KLVF 4  
DB 6 KLVF 9  
  
RESULT 8  
O9GR26 PRELIMINARY; PRT; 48 AA.  
ID O9GR26  
AC O9GR26;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Elongation factor-1alpha (Fragment).  
GN EF-1ALPHA.  
OS Aphidius colemani (Aphid parasite).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
OC Ichneumonidae; Braconidae; Aphidinae; Aphidius.  
OX NCBI\_TaxID=78482;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sanchez A., Belshaw R., Michelena J., Latorre A., Quicke D.,  
RA Gardiner U.;  
RT "The phylogenetic analysis of variable length sequence data: elongation  
RT factor-1alpha introns in European populations of the parasitoid wasp

RT Pauesia (Hymenoptera: Braconidae: Aphidiinae).";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ401978; CAC19825.1; -  
FT NON TER 1  
FT NON TER 48 48  
SQ SEQUENCE 48 AA; 5593 MW; 5FF20AA7979B6D16 CRC64;

Query Match 100.0%; Score 4; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 32 KLVF 35

## RESULT 9

Q8QMN2 PRELIMINARY; PRT; 51 AA.

AC Q8QMN2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE V206.

OS Cowpox virus (CPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10243;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRIGHTON RED;  
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;  
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of repeated and unique sequence elements.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116 (1982).  
RN [2]

RN SEQUENCE FROM N.A.  
RC STRAIN=BRIGHTON RED;  
RX MEDLINE=90177240; PubMed=2309453;  
RA Parsons B.L., Pickup D.J.;  
RT "Transcription of orthopoxvirus telomeres at late times during infection.";  
RL Virology 175:69-80 (1990).  
RN [3]

RN SEQUENCE FROM N.A.  
RC STRAIN=BRIGHTON RED;  
RX MEDLINE=91196263; PubMed=2014645;  
RA Hu F.Q., Pickup D.J.;  
RT "Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution.";  
RL Virology 181:716-720 (1991).  
RN [4]

RN SEQUENCE FROM N.A.  
RC STRAIN=BRIGHTON RED;  
RX MEDLINE=94378510; PubMed=8091665;  
RA Hu F.Q., Smith C.A., Pickup D.J.;  
RT "Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor.";  
RL Virology 204:343-356 (1994).  
RN [5]

RN SEQUENCE FROM N.A.  
RC STRAIN=BRIGHTON RED;  
RA Pickup D.J.;  
RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.  
RN [6]

RN SEQUENCE FROM N.A.  
RC STRAIN=BRIGHTON RED;  
RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF482758; AAM13654.1; -  
SQ SEQUENCE 51 AA; 6002 MW; 97429938CAB1D4B5 CRC64;

Query Match 100.0%; Score 4; DB 12; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 16 KLVF 19

## RESULT 10

Q9MEHO PRELIMINARY; PRT; 52 AA.

AC Q9MEHO;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE NADH dehydrogenase subunit 1 (Fragment).

GN NDI.  
OS Meganyctiphanes norvegica.  
OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Euphausiacea; Euphausiidae; Meganyctiphanes.  
OX NCBI\_TaxID=48144;  
RN [1]

RP SEQUENCE FROM N.A.

RA Zane L., Ostelli L., Maccatrozzo L., Bargelloni L., Cuzin-Roudy J.,  
RA Buchholz F., Patarnello T.;  
RT "Genetic differentiation in a pelagic crustacean (Meganyctiphanes norvegica, Euphausiacea) from the North East Atlantic and the Mediterranean Sea";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF150623; AAF73171.1; -  
DR EMBL; AF150612; AAF73160.1; -  
DR EMBL; AF150613; AAF73161.1; -  
DR EMBL; AF150614; AAF73162.1; -  
DR EMBL; AF150615; AAF73163.1; -  
DR EMBL; AF150616; AAF73164.1; -  
DR EMBL; AF150617; AAF73165.1; -  
DR EMBL; AF150618; AAF73166.1; -  
DR EMBL; AF150619; AAF73167.1; -  
DR EMBL; AF150620; AAF73168.1; -  
DR EMBL; AF150621; AAF73169.1; -  
DR EMBL; AF150622; AAF73170.1; -  
DR InterPro; IPR001694; Resp\_NADH\_dhl.  
DR Pfam; PF00146; NADHdh; 1.

KW Mitochondrion.

FT NON TER 1 1

FT NON TER 52 52

SQ SEQUENCE 52 AA; 6120 MW; 041571A67AF9D16D CRC64;

Query Match 100.0%; Score 4; DB 8; Length 52;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
Db 27 KLVF 30

## RESULT 11

Q8RBV2 PRELIMINARY; PRT; 54 AA.

AC Q8RBV2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical protein TTE0706.

GN TTE0706.

OS Thermoanaerobacter tengcongensis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.  
OX NCBI\_TaxID=119072;  
RN [1]



RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4T / JCM11007;  
 RX MEDLINE=21992816; PubMed=11997336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,  
 RT "A complete sequence of *T. tengcongensis* genome.";  
 RL Genome Res. 12:689-700(2002).  
 DR EMBL; AF013039; AAM23968.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 54 AA; 6436 MW; 7EA021E52840EC15 CRC64;

Query Match 100.0%; Score 4; DB 16; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 DB 7 KLVF 10

RESULT 12  
 ID 0921T0 PRELIMINARY; PRT; 57 AA.  
 AC 0921T0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical protein RC0340.  
 GN RC0340.  
 OS *Rickettsia conorii*.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MALISH 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samuel D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.,  
 RT Mechanisms of evolution in *Rickettsia conorii* and *R. prowazekii*.  
 RL Science 293:2093-2098(2001).  
 DR EMBL; AF008599; AAL02878.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 57 AA; 6509 MW; 43A414C10AE77085 CRC64;

Query Match 100.0%; Score 4; DB 16; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 DB 52 KLVF 55

RESULT 13  
 ID 039633 PRELIMINARY; PRT; 58 AA.  
 AC 039633;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Capsid protein (Fragment).  
 OS Calicivirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae.  
 OX NCBI\_TaxID=11975;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LYMINGTON/94/UK;  
 RX MEDLINE=97278118; PubMed=9131452;  
 RA Green S.M., Lambden P.R., Owen Caul E., Clarke I.N.,  
 RT "Capsid sequence diversity in small round structured viruses from

RT recent UK outbreaks of gastroenteritis.";  
 RL J. Med. Virol. 52:14-19(1997).  
 DR EMBL; Z73995; CAA98301.1; -;  
 DR InterPro; IPR004005; Calici\_coat.  
 DR Pfam; PF00915; Calici\_coat\_1.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 58 AA; 6159 MW; A2D51FD32B3B5EA1 CRC64;

Query Match 100.0%; Score 4; DB 12; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 DB 18 KLVF 21

RESULT 14  
 ID 09AF20 PRELIMINARY; PRT; 61 AA.  
 AC 09AF20;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE IS91 orfA.  
 GN S0020.  
 OS *Shigella flexneri*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TaxID=623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21189246; PubMed=11292750;  
 RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,  
 RA Blattner F.R.,  
 RT "Complete DNA sequence and analysis of the large virulence plasmid of  
 RT *Shigella flexneri*.";  
 RL Infect. Immun. 69:3271-3285(2001).  
 DR EMBL; AF348706; AAK18331.1; -;  
 KW Plasmid.  
 SQ SEQUENCE 61 AA; 6864 MW; 49C34FBA7EBDC228 CRC64;

Query Match 100.0%; Score 4; DB 2; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
 DB 7 KLVF 10

RESULT 15  
 ID 08W6C9 PRELIMINARY; PRT; 62 AA.  
 AC 08W6C9;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE MemB.  
 GN ORF62.  
 OS Vibrio phage VSK.  
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.  
 OX NCBI\_TaxID=181604;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Basu N., Kar S., Ghosh R.K.,  
 RT "Molecular analysis of filamentous phage VSK of *Vibrio cholerae* 0139:  
 RT A possible clue to genetic transmissibility.";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF453500; AAL49745.1; -;  
 SQ SEQUENCE 62 AA; 7221 MW; 56813397E7BC2BDF CRC64;

Query Match 100.0%; Score 4; DB 9; Length 62;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
Db 19 KLVP 22

RESULT 16  
Q8SPJ7 PRELIMINARY; PRT; 63 AA.  
AC Q8SPJ7;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Glutamate-ammonia ligase [EC 6.3.1.2] (Fragment).  
GN GLUL.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LARGE WHITE BREED;  
RA Stratil A., Kubickova S., Archibald A.L., Peelman L.J., Musilova P.,  
RA Van Poucke M., Rubes J.;  
RT "FISH, RH and linkage mapping of the porcine GLUL gene to the distal  
RT end of chromosome 9q."; to the EMBL/GenBank/DBJ databases.  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ430415; CAD23065.1; -.  
KW Ligase.  
FT NON TER 1  
FT NON TER 63  
SQ SEQUENCE 63 AA; 7327 MW; EB32B03A687CDE73 CRC64;

Query Match 100.0%; Score 4; DB 6; Length 63;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
Db 35 KLVP 38

RESULT 17  
Q9NH7 PRELIMINARY; PRT; 64 AA.  
AC Q9NH7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Hypothetical 7.1 kDa protein (Fragment).  
GN ANON-EST:f2E21.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON-S;  
RA Schmid K.J., Tautz D.;  
RT "A screen for rapidly evolving genes from Drosophila.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF217401; AAF73386.1; -.  
DR FlyBase; FBgn025221; anon-EST:f2E21.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 64 AA; 7088 MW; 111238D2DDA2A8DF CRC64;

Query Match 100.0%; Score 4; DB 5; Length 64;

Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
Db 40 KLVP 43

RESULT 18  
Q94144 PRELIMINARY; PRT; 65 AA.  
AC Q94144;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Rab6-like (Fragment).  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nonet M.L., Staunton J.E., Kilgard M.P., Fergestad T., Jorgensen E.,  
RA Hartweig E., Horvitz H.R., Meyer B.J.;  
RT "Functional synapses that are partially depleted of vesicles in C.  
RT elegans rab-3 mutants."; to the EMBL/GenBank/DBJ databases.  
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U68253; AAB16968.1; -.  
DR InterPro; IPR001806; Ras.trnsfrmng.  
DR InterPro; IPR003575; Small\_GTPase.  
DR Pfam; PF00071; ras; 1.  
DR PRINTS; PR00449; RASTRNSFRMNG.  
DR SMART; SM00010; small\_GTPase; 1.  
KW GTP-binding.  
FT NON TER 65  
SQ SEQUENCE 65 AA; 7637 MW; E4A9042D6050B828 CRC64;

Query Match 100.0%; Score 4; DB 5; Length 65;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4  
Db 13 KLVP 16

RESULT 19  
Q92IF4 PRELIMINARY; PRT; 67 AA.  
AC Q92IF4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical protein RC0466.  
GN RC0466.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MALISH 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098 (2001).  
RL EMBL; AE008610; AAL03004.1; -.  
DR Hypothetical protein; Complete proteome.  
SQ SEQUENCE 67 AA; 7384 MW; 4D408968208B0348 CRC64;

Query Match 100.0%; Score 4; DB 16; Length 67;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 5 KLVF 8

## RESULT 20

Q9SMP2 PRELIMINARY; PRT; 69 AA.

AC Q9SMP2; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE Protein translocation complex sec61 gamma chain-like protein.  
GN T8P19.80.

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;

RA Choiane N., Robert C., Brottier P., Wincker P., Catolico L.,  
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X., Queirer F., Salanoubat M.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL13315; CAB62346.1; -;  
DR InterPro; IPR001901; SECC.

DR InterPro; IPR004795; SECC\_euk\_arch.

DR Pfam; PF00584; SECC; 1.

DR ProDom; PD010355; SECC\_euk\_arch; 1.

DR TIGR/Pfam; TIGR00327; SECC\_euk\_arch; 1.

SO SEQUENCE 69 AA; 7683 MW; 4963D6EB8BC875CE CRC64;

Query Match 100.0%; Score 4; DB 10; Length 69;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 55 KLVF 58

## RESULT 21

Q8UC16 PRELIMINARY; PRT; 71 AA.

AC Q8UC16; 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DE Hypothetical protein At2G2501.

GN AT2G2501.

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI\_TaxID=176299;

RA SEQUENCE FROM N.A.

RP MEDLINE=21608550; PubMed=11743193;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,  
RA Chapman P., Clendinning J., Decherage G., Giller W., Grant C.,  
RA Kutayev T., Levy R., Li M.-J., McClelland E., Palmeri A.,  
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Nester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
RT C58.";  
RL Science 294:2317-2323 (2001).  
DR EMBL; AE009196; AA143488.1; -;  
KW Hypothetical protein; Complete proteome.  
SO SEQUENCE 71 AA; 8039 MW; C5AF76D190B51312 CRC64;

Query Match 100.0%; Score 4; DB 16; Length 71;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 45 KLVF 48

## RESULT 22

Q25925 PRELIMINARY; PRT; 72 AA.

AC Q25925; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE Major surface antigen (P190) (Fragment).

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=5833;

RA SEQUENCE FROM N.A.

RP MEDLINE=85012680; PubMed=6090934;

RA Hall R., Hyde J.E., Goman M., Simmons D.L., Hope I.A., Mackay M.,  
RA Scaife J.;

RT "Major surface antigen gene of a human malaria parasite cloned and  
RT expressed in bacteria.";

RL Nature 311:379-382 (1984).

DR EMBL; M32152; AAA29658.1; -;

FT NON TER 1 1

SO SEQUENCE 72 AA; 8451 MW; 14B8A903D13F1AA5 CRC64;

Query Match 100.0%; Score 4; DB 5; Length 72;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 38 KLVF 41

## RESULT 23

Q936G7 PRELIMINARY; PRT; 74 AA.

AC Q936G7; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE Trans-golgi membrane protein p230.

GN Staphylococcus aureus.

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Staphylococcus.

OX NCBI\_TaxID=1280;

RA SEQUENCE FROM N.A.

RP MEDLINE=95050273; PubMed=7961465;

RA Lin W.S., Cumteen T., Lee C.Y.;

RT "Sequence analysis and molecular characterization of genes required  
RT for the biosynthesis of type 1 capsular polysaccharide in  
RT Staphylococcus aureus.";

RL J. Bacteriol. 176:7005-7016 (1994).

RA SEQUENCE FROM N.A.

RP

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RC STRAIN=M;
RA Luong T.T., Shu O., Bush K., Lee C.Y.;
RT "The Type Capsular Polysaccharide of Staphylococcus aureus is carried
in a Staphylococcal Cassette Chromosome Genetic Element.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10927; AAL26671.1; -. F725CA086873396B CRC64;
SQ SEQUENCE 74 AA; 8764 MW; 725CA086873396B CRC64;

Query Match 100.0%; Score 4; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 53 KLVP 56

RESULT 24
Q8VVM4 Q8VVM4 PRELIMINARY; PRT; 76 AA.
AC Q8VVM4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE YggE protein (Fragment).
GN YGGE.
OS Escherichia coli.
OG Plasmid pCMXR1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HKYM68;
RA Doi Y., Shibata N., Arakawa Y.;
RT "Escherichia coli plasmid pCMXR1 integron, ampC gene (beta-lactamase
CMY-9), aacAI gene, strain HKYM68.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB061794; BAB72160.1; -.
DR InterPro; IPR003774; DUF179.
DR Pfam; PF02622; DUF179; 1.
KW Plasmid.
FT NON TER
SQ SEQUENCE 76 AA; 8191 MW; 3439EA9887DD96CB CRC64;

Query Match 100.0%; Score 4; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 44 KLVP 47

RESULT 25
Q9TBS6 Q9TBS6 PRELIMINARY; PRT; 76 AA.
AC Q9TBS6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
OS Toxostoma longirostre.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.
OX NCBI_TaxID=99880;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LBTH4TX;
RA Zink R.M., Dittmann D.L., Klicka J., Blackwell-Rago R.C.;
RT "Evolutionary patterns of morphometrics, allozymes and mitochondrial
DNA in thrashers (Toxostoma).";
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RL Auk 0:0-0(1999).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF154428; AAD56150.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER
SQ SEQUENCE 76 AA; 8241 MW; 26D8D80FC092B356 CRC64;

Query Match 100.0%; Score 4; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 6 KLVP 9

RESULT 26
Q9TBS2 Q9TBS2 PRELIMINARY; PRT; 76 AA.
AC Q9TBS2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN ND2.
OS Toxostoma rufum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.
OX NCBI_TaxID=58210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRTH3LA;
RA Zink R.M., Dittmann D.L., Klicka J., Blackwell-Rago R.C.;
RT "Evolutionary patterns of morphometrics, allozymes and mitochondrial
DNA in thrashers (Toxostoma).";
RL Auk 0:0-0(1999).
CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF154440; AAD56154.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER
SQ SEQUENCE 76 AA; 8229 MW; 2769681FC193B256 CRC64;

Query Match 100.0%; Score 4; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVP 4
Db 6 KLVP 9

RESULT 27
Q54879 Q54879 PRELIMINARY; PRT; 77 AA.
AC Q54879;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ExciGionase.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE OF 61-77 FROM N.A.
RC STRAIN=SP1000; TRANSPOS=TN5252;
EX MEDLINE=94327488; PubMed=8051031;
RA Kilic A.O., Vijayakumar M.N., al-Khalidi S.F.;
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RT "identification and nucleotide sequence analysis of a transfer-related  
RT region in the streptococcal conjugative transposon Tns252." ;  
RL J. Bacteriol. 176:5145-5150(1994).  
RN [2]  
RP SEQUENCE OF 1-61 FROM N.A.  
RC STRAIN=SP1000; TRANSPOSON=TN5252;  
RA Srinivas P., Vijayakumar M.N.;  
RT "A regulatory region in streptococcal conjugative transposon Tns252." ;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L29324; AAC98430.1; -  
SQ SEQUENCE 77 AA; 9631 MW; 2713BL3BB2160829 CRC64;

Query Match 100.0%; Score 4; DB 2; Length 77;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 56 KLVF 59

RESULT 28  
Q9HPR1 PRELIMINARY; PRT; 78 AA.  
AC Q9HPR1;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Vng1513h.  
GN VNG1513h.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahaitas G.G., Bergquist B., Pan M.,  
RA Shukla H.D., Laskey S.R., Baliga N.S., Thorsson V., Shrogha J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Meliti R., Goo Y.A.,  
RA Leitman B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonki P.E., Krebs W.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Peck R.F., Pohlschoder M., Spudich J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasgupta S.;  
RT "Genome sequence of Halobacterium species NRC-1." ;  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AB05065; AAG19806.1; -  
KW Complete proteome.  
SQ SEQUENCE 78 AA; 8450 MW; A5AE2251CEB803E5 CRC64;

Query Match 100.0%; Score 4; DB 17; Length 78;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 40 KLVF 43

RESULT 29  
Q969F3 PRELIMINARY; PRT; 79 AA.  
AC Q969F3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Capring protein (actin filament) muscle Z-line, beta.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC012305; AAH12305.1; -  
DR EMBL; BC008095; AAH08095.1; -  
SQ SEQUENCE 79 AA; 8747 MW; F1D795811CA4D556 CRC64;

Query Match 100.0%; Score 4; DB 4; Length 79;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 22 KLVF 25

RESULT 30  
O35463 PRELIMINARY; PRT; 79 AA.  
AC O35463;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Alzheimer's amyloid beta protein (fragment).  
GN BETA APP.  
OS Cricetus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sambumuti K., Pinnix I., Gandhi S.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF030413; AAB86608.1; -  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
FT NON\_TER 1 79  
FT NON\_TER 1 79  
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BF3F597 CRC64;

Query Match 100.0%; Score 4; DB 11; Length 79;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4  
DB 36 KLVF 39

RESULT 31  
Q92GT7 PRELIMINARY; PRT; 79 AA.  
AC Q92GT7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical protein KC1035.  
GN KC1035.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MALISH 7;

```
RX MEDLINE=2142074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008655; AA03573.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 79 AA; 9510 MW; 19F65AB63FDFAEA7 CRC64;

Query Match 100.0%; Score 4; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KLVF 4
Db 39 KLVF 42

RESULT 32
O96183 PRELIMINARY; PRT; 81 AA.
AC O96183
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein translocation complex, sec61 gamma chain.
GN PF00450W.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551;
RA Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shalton S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
falciparum.";
RL Science 282:1126-1132(1998).
DR EMBL; AE001395; AAC71879.1; -.
DR InterPro; IPR001901; SecE.
DR InterPro; IPR004795; SecE_euk_arch.
DR Pfam; PF00584; SecE; 1.
DR ProDom; PD010355; SecE_euk_arch; 1.
DR TIGRFAMs; TIGR00327; secE_euk_arch; 1.
SQ SEQUENCE 81 AA; 9286 MW; AD7A3302A76191E9 CRC64;

Query Match 100.0%; Score 4; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KLVF 4
Db 67 KLVF 70

RESULT 33
Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

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RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 4; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KLVF 4
Db 33 KLVF 36

RESULT 34
Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50B5E79230A CRC64;

Query Match 100.0%; Score 4; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 KLVF 4
Db 33 KLVF 36

RESULT 35
Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 4; Length 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 33 KLVF 36

RESULT 36
P78438 PRELIMINARY; PRT; 82 AA.
ID P78438;
AC P78438;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amyloid protein (Beta-amyloid protein) (Fragment).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnson E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN 2;
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gueella J.F., Watkins P.C., Brune G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN 3;
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93053597; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijeman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 4; Length 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KLVF 4
Db 32 KLVF 35

RESULT 37
Q8UC93 PRELIMINARY; PRT; 83 AA.
ID Q8UC93;
AC Q8UC93;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein Atu2605.
GN ATU2605.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gilliet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao J., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AB009207; AAL43586.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 83 AA; 9653 MW; 364F3CBA1FDF40AB CRC64;

Query Match
Best Local Similarity 100.0%; Score 4; DB 16; Length 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVF 4
Db 3 KLVF 6

RESULT 38
Q8YH11 PRELIMINARY; PRT; 84 AA.
ID Q8YH11;
AC Q8YH11;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BMEI0993.
GN BMEI0993.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapactral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Iykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

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DR EMBL; AE009540; AAL52174.1; --  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 84 AA; 9641 MW; D20FB5DF78D6E603 CRC64;

Query Match 100.0%; Score 4; DB 16; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 ||||  
 Db 13 KLVF 16

## RESULT 39

Q9TBS4 Q9TBS4 PRELIMINARY; PRT; 85 AA.  
 AC Q9TBS4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN ND2.  
 OS Toxostoma guttatum.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.  
 OX NCBI\_TaxID=99879;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COZ1;  
 RA Zink R.M., Dittmann D.L., Klicka J., Blackwell-Rago R.C.;  
 RT "Evolutionary patterns of morphometrics, allozymes and mitochondrial  
 RT DNA in thrashers (Toxostoma).";  
 RL Auk 0:0-0(1999).  
 CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.  
 DR EMBL; AF154434; AAD56152.1; --  
 DR InterPro; IPR001750; Oxidored\_q1.  
 DR Pfam; PF00361; oxidored\_q1; 1.  
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.  
 FT NON\_TER 1  
 FT NON\_TER 85  
 SQ SEQUENCE 85 AA; 9388 MW; 3AB9612E547BB534 CRC64;

Query Match 100.0%; Score 4; DB 8; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 ||||  
 Db 15 KLVF 18

## RESULT 40

Q9TBS0 Q9TBS0 PRELIMINARY; PRT; 85 AA.  
 AC Q9TBS0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN ND2.  
 OS Toxostoma ocellatum.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.  
 OX NCBI\_TaxID=99881;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OCTH2MX;  
 RA Zink R.M., Dittmann D.L., Klicka J., Blackwell-Rago R.C.;  
 RT "Evolutionary patterns of morphometrics, allozymes and mitochondrial  
 RT DNA in thrashers (Toxostoma).";  
 RL Auk 0:0-0(1999).

CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.  
 DR EMBL; AF154446; AAD56156.1; --  
 DR InterPro; IPR001750; Oxidored\_q1.  
 DR Pfam; PF00361; oxidored\_q1; 1.  
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.  
 FT NON\_TER 1  
 FT NON\_TER 85  
 SQ SEQUENCE 85 AA; 9330 MW; 2786E1C2B12BE2A1 CRC64;

Query Match 100.0%; Score 4; DB 8; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVF 4  
 ||||  
 Db 15 KLVF 18

Search completed: January 3, 2003, 07:53:05  
 Job time : 62 secs